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CryoWEB – User's Guide and Reference Manual

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Preface

The United Nations proclaimed 2010 to be the International Year of Biodiversity. Therefore, the publication of this CryoWEB Users Guide comes at a very appropriate time. Genebanks have a long tradition in particular in plants, and have formed an integral part of plant breeding in agriculture. Slowly, they are also being established in animal agriculture for the conservation of the abundance of breeds created by animal breeders worldwide. Every such genebank needs a documentation system, without which it would be useless. And here is where CryoWEB comes into the picture. If already the setup of a genebank is wrought with problems, organizational and legal issues, CryoWEB attempts to at least relieve their initiators of the worry about documenting the content of the newly established genebanks.

The EFABISnet project, funded by the European Union, made it possible to install CryoWEB in 14 European countries, with an additional installation in Vietnam. This demonstrates the general utility of the package. While these installations have been accompanied by training workshops, further use requires sufficient documentation. This need is intended to be covered by the book presented here.

While this contribution is all about documentation, its object, i.e., the software had to be created in the first place. Therefore, it seems appropriate to acknowledge the trail of CryoWEB developers, trail, because it has gone through a whole series of moults until it finally reached its current WEB based shape. These are Lina Yordanova, Truong Van Chi Cong and Zhivko Duchev, all of them working at one time or the other at the Department of Animal Breeding and Genetic Resources.

Although online documentation is spreading (also CryoWEB utilizes this technique), it was felt that proper printed documentation is often more efficient and therefore preferred, prompting us to write this book. Nonetheless, distribution of this document shall be largely electronic, but can be printed and bound afterwards. In this way, Gutenberg's 15th century invention can coexist very well with its 21st century successors.

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Mariensee May 2010

Contents

8 Administrator's tasks 113

1 Introduction

In the wake of the Rio Convention [8] and, in particular after the adoption of the Interlaken Declaration, the setup of genebanks in animal agriculture has become an accepted high priority objective. A diverse range of materials can be used for cryogenic backup, such as semen, embryos, oocytes, and somatic cells, differing in complexity and costs of collection. Often, the setup of a genebank will be a national endeavor, as it can be viewed as a repository of a country's genetic heritage. While the condition and operations of national genebanks will be very different from one country to the next, all of them require a system for documentation. This is where CryoWEB comes into the picture: it has been developed as the documentation component of the concept for a world wide emergency program for the setup of genebanks [4]. Wherever genebanks are setup in animal agriculture, CryoWEB is intended to be used as an out of the box system for managing such repositories.

1.1 Prerequisites

CryoWEB is a fully fledged WEB application which means that it is not just one executable program but rather a complete computer system consisting of an operating system, a database and web server and the CryoWEB, and loads of other Open Source software. While this may sound intimidating under installation aspects, latest virtualization technology will make installation a breeze. Such a virtual system is called appliance which presents itself to the users as one very big file. To be able to run it, a computer with sufficient RAM and disk space is required. This can be either a Linux or Windows system which will serve as a host system to the CryoWEB appliance, which is effectively a complete Linux system running on top of the host. Therefore, a multiprocessor system would be a good starting point.

CryoWEB is accessed exclusively through web browsers. Therefore, CryoWEB should have access to the web or a local area network (LAN). Then all users on that network can access the system. If only limited access is required, the one stand alone computer will also work, and the LAN requirement can be dropped.

Being the sole documentation system of a genebank, care must be taken to ensure no data is lost. Thus, another prerequisite is a backup system.

A final, and perhaps the most taxing requirement for running CryoWEB, is a dedicated person, who really knows the genebank and the implications long term data storage and retrieval carries with itself. This holds in particular for the issue of having to develop, define and enforce policies on data entry that have already been mentioned.

1.2 Target audience

To be able to install, maintain and operate CryoWEB, three groups of persons need to work together. These are the system administrator of the operating system (sysadmin-OS), the administrator of CryoWEB (admin-CryoWEB) and the person who regularly uses CryoWEB on a daily basis (user-CryoWEB). This publication contains all information for the above mentioned three activity groups. Thus, it is intended to be sufficiently detailed to allow installation, operation and maintenance of CryoWEB without any additional sources. Ideally, a new prospective user would participate in a one week CryoWEB course, which have been run a number of times. However, the three components CryoWEB appliance, this book and sufficient time to study the latter should be enough to set up and run the documentation system for genebanks.

To this effect, the chapters “Installation of CryoWEB” and “Maintenance of the CryoWEB system” are intended for sysadmin-OS, i.e. for the system and database administrator, who is usually an IT person managing the computer network and backups.

CryoWEB is made available in English, but has been designed to be translated into other languages. This process is described in the chapter “Nationalization of CryoWEB”. This process has to be performed by the sysadmin-OS and the admin-CryoWEB, as it involves IT and cryo bank issues. Furthermore, if large amounts of historic data are already available in some electronic format, it may make sense to load this data through programs as described in the chapter “Loading historic data”. For this task an IT person with programming expertize will be required additional to the admin-CryoWEB.

Next, the chapter “Administrator tasks” deals with the internal management aspects of CryoWEB, like creating new users, defining breeds etc., tasks to be done by the admin-CryoWEB. Thirdly, the user entering the data, i.e. the user-CryoWEB will mostly be concerned with the chapters “User tasks”. Often, the latter two will be the same person. All the other texts should be read by everyone, as they set the scene (“Introduction”, “CryoWEB overview”) or provide explanation in case errors are encountered (“Error messages”).

1.3 Introduction to National genebanks

National genebanks are repositories of genetic material stored in liquid nitrogen at -196°C. At this temperature, the genetic material can be stored indefinitely, and after thawing, following an appropriate protocol, be introduced in animal breeding. For semen, this procedure is straight forward, following every day practice. Implanting embryos is somewhat more involved, but also a standard practice in many species, while the reconstitution of animals through nuclear transfer and cloning on the basis of somatic cells is still tedious and expensive.

National genebanks require a formal and even legal framework for operation, which deals with ownership issues of the stored material and access to it. Often, core material of a genebank cannot be removed, while surplus material may be shared with interested parties. CryoWEB supports differential status of material, however, the policies have to be developed and determined within each individual genebank. There is one chapter on “Policies” that points the prospective user to the issues, listing a number of decisions that need to be taken.

Often genebank material is stored in different locations. This may be for security reasons, but also due to organizational issues, as different organizations may be responsible for local genebank material, resulting in a distributed genebank. CryoWEB supports this by allowing a five level storage scheme.

National genebanks are setup with the explicit intention to last a long time. This implies that it will have to operate under changing conditions. Accordingly, the set of rules applicable to a genebank may be different to, e.g., an Artificial Insemination center’s cryo storage facility, which supplies semen on a regular and daily basis.

Then the criterion of long term storage impacts on the sanitary rules of the material, also data collected on them will have to stand the test of time, i.e. be available for extended period.

1.4 CryoWEB overview

With the international acceptance of the so called Rio Convention [8] in 1992, conservation of biodiversity has become a major issue not only in wild life, but also in animal agriculture. While conservation in wild life usually focuses on the species, breeds are the focus of interest in animal agriculture. Already in 1979 scientists stipulated conservation of breeds of farm animals [3].

Contrary to animal agriculture, plants genebanks have been in operation for a long time. Consequently, documentation has also been developed [1].

More recently, a proposal was made for a world wide emergency program for the creation of National genebanks of endangered breeds in animal agriculture [5] based on the low cost collection and storage of somatic cells. The sampling technique was tested under field conditions on 6 breeds from 3 species [4]. The procedure is intended to be deployed rapidly to countries with little infrastructure, and to operate identically on all mammalian species. An integral part of a physical genebank is sufficient documentation of the stored samples, which has to be equally easy and rapid to install and operate, and which only requires limited or no adaptation prior to country installation. Based on the implementation for the National Genebank in the Netherlands [6], the structure of the new system was further simplified to allow general applicability without modification.

1.5 Design Objectives

The design objectives are to be derived from the intended user areas.

1.5.1 Intended User Areas

As pointed out above, CryoWEB is considered to be a component in the concept for a world wide emergency program for the setup of genebanks. Implementation of this program would entail setting up a relatively large number of national and possibly sub-national genebanks. Clearly, a standardized product, that does not require software expertize for adaptation would be of great benefit.

Often multiple locations are used in genebanks. Firstly, there are safety issues that make it advisable to store material in more than one location. Furthermore, a decentralized approach in terms of material and data collection may seem advisable. Clearly, information on all genebank material, be it centralized or not, needs to be available together.

The information available on animals from which material is put in cryo store will be very different ranging from complete pedigrees and performance records for some populations in intensive breeding programs to close to none on animals sampled in remote low intensity environments. The system must be able to handle both cases without modification.

1.5.2 Functionality

The basic objective is to provide a register for the material stored in the genebank. The main requirements are:

1. The identification on the vessel must be unique in the genebank and lead directly to the information about it in the database. This means, that any sample taken out of the genebank must lead solely through its vessel identification to information about it in the database.
2. The information in the database about a sample in the genebank must lead directly to the actual sample in the physical store. This means, that a record about a sample in the database must, through its location information, lead directly to the correct vessel in the genebank store.
3. The application must have the capability to be nationalized.
4. The database should be accessible through the Internet, allowing centralized and non centralized data entry.
5. The system should be usable for all possible genetic materials (semen, oocytes, embryos, somatic cells, DNA, blood) and all possible types of used vessels (straw, tube, cane, vial, ampule) in a uniform manner.
6. For sanitary reasons, the history of all material movements in the physical store should be recorded.
7. The database should store a minimum amount of information for the materials, that is expected to be needed and available for the next decade.
8. The information stored should be uniformly available across all species and populations.

9. From its content and operations CryoWEB has to be able to be run for an extended time span as is appropriate for long term genebanks.

The rational for some of the objectives has been outlined in Groeneveld [4]

1.6 Notation conventions

Throughout this manual, the specific items of information are referred to in the following ways:

- Menu items/Icons/Buttons that should be clicked/selected in a workflow procedure are presented as follows:
  Click **Search** button. The **Submit** button label will change to **Delete**.
- The sequence of items to be clicked are indicated by the menu entries separated by "▷", e.g. Open the **Protocols** page via **Main Menu** ▷ **Cryo material** ▷ **Protocols**.
- Web addresses are shown as: `http://cryoweb.tzv.fal.de/`
- File names are written in Typewriter font family, e.g. `C:\vmware\CryoWEB\CryoWEB.vmdk`.
- Settings files and system messages are shown in boxes, e.g.

```
# Locale  for samples_statistics.jrxml
r001.title=Animal Samples Report
r001.animal_code=Animal ID
r001.species=Species
```

- Important points in the text, like layout names, field names, or policy elements are highlighted either as: *type of vessel* or **Donor**.
- Notes are shown in ovals:

Note: On each menu click the CryoWEB connects to the server to generate the form with the last data available at the moment. Depending on the speed of your Internet connection, it may take some time before the form is shown and filled with data.

2 The CryoWEB screen layout

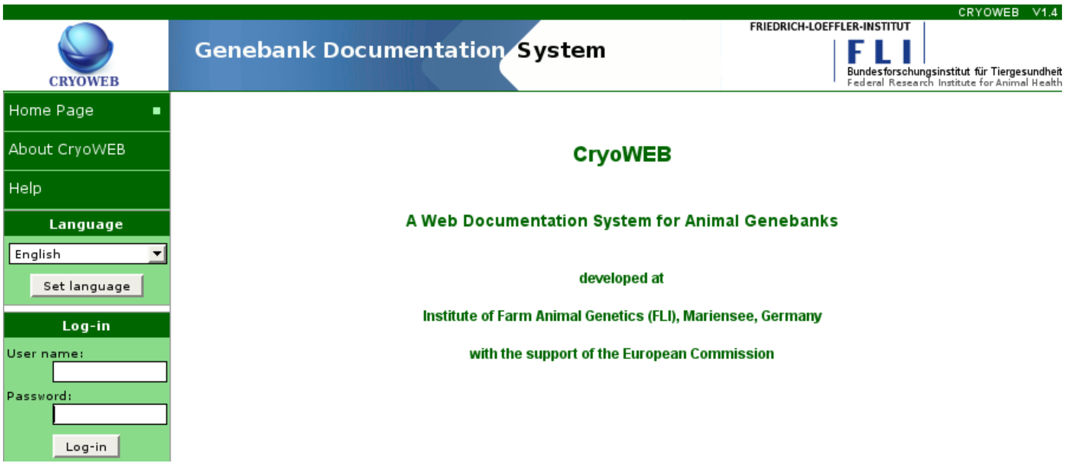
All user and administration interaction with CryoWEB is done through the browser interface, except for the loading of historic data, that some users may perform in the initial migration process from an already existing electronic data format to CryoWEB as described in Chapter 5.4.

Most of the forms in CryoWEB follow a uniform layout that is described in the next sections.

2.1 Login screen

When you open the CryoWEB page in your browser, the first screen you see is the initial login screen (Figure 2.1). On the top of the page is the standard **CryoWEB banner**, below it on the left side are the **Language** and **Log-in** block.

Two actions can be executed on the login screen - selection of the interface language and logging into the system.



CryoWEB

A Web Documentation System for Animal Genebanks

developed at

Institute of Farm Animal Genetics (FLI), Mariensee, Germany

with the support of the European Commission

Figure 2.1: The initial login screen of CryoWEB

2.1.1 Selection of interface language

The default interface language in CryoWEB is English. However, the interface is usually localized in the official national language (see the nationalization section). Thus, before logging into the system, the user has to choose the interface language.

This is done by selecting an entry from the **Language** drop-down list and clicking the **Set language** button. The login screen remains unchanged, but after the user signs in with her user name and password, the interface will be shown in the chosen language. Once logged in the user cannot change the interface language until the next login.

2.1.2 User accounts

The content of the national genebank is protected from the general public and available only to restricted group of users. These users are registered with the national genebank manager and must receive from her their personal access account (user name and password). Only after logging into the system the user gets access to the data and the web interface.

Four groups of users are predefined in CryoWEB. Each group has access to read all the data, but only restricted access for data modification. The groups are:

Guests - this group can only read the data and is not allowed to make any modifications. It is intended for persons who will only read the data from the national genebank, e.g. for monitoring conservation programmes.

Operators - this is the standard group for the users who will routinely enter data. This group can read and modify all the data except the administration part, i.e. the operators cannot add new breeds or change the name of a vessel type. The operators have access to all samples and animal data, i.e. each operator can modify the data for each animal and sample.

Managers - this group has all the privileges of the operator and, additionally, can enter and modify data in the administration part - add new species, breeds, vessel types. The managers can link breeds to species names and CryoWEB breeds to EFABIS breeds, and export data for EFABIS[7, 2]. The exported data are the total numbers of cryopreserved material samples per breed and year, aggregated by material type. Such feature is useful for the National Coordinators for management of farm animal genetic resources who are supposed to report such kind of data on European level.

Administrators - this group has the full access to the data and can make any data modifications. The members of this group have the permissions to manage also the users data - create new users, give certain access rights to a user, etc. When a new user needs to receive access to CryoWEB, a member of the administrator's group has to register this user in the Access Rights Manager, create user name and passwords and provide them to the user.

2.2 General page layout

After the login process the home page is shown (Figure 2.2). The top of the page displays the standard banner, with the **CryoWEB logo** on the left side. Right below it, on the dark green background, we find the menu area with five options, followed by the status area (light green background) containing details about the user. The remaining area with the white background is the primary place where the data entry forms will be shown.

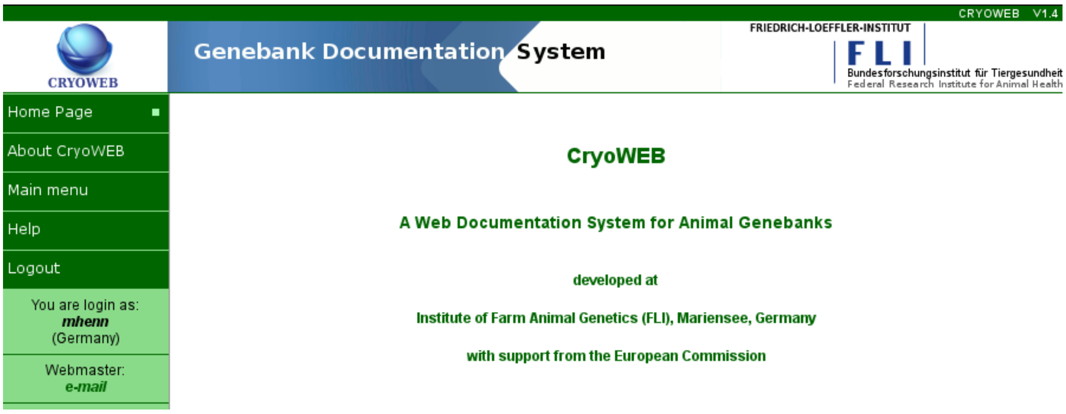


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Figure 2.2: The home page of CryoWEB

In the menu area the following options are available:

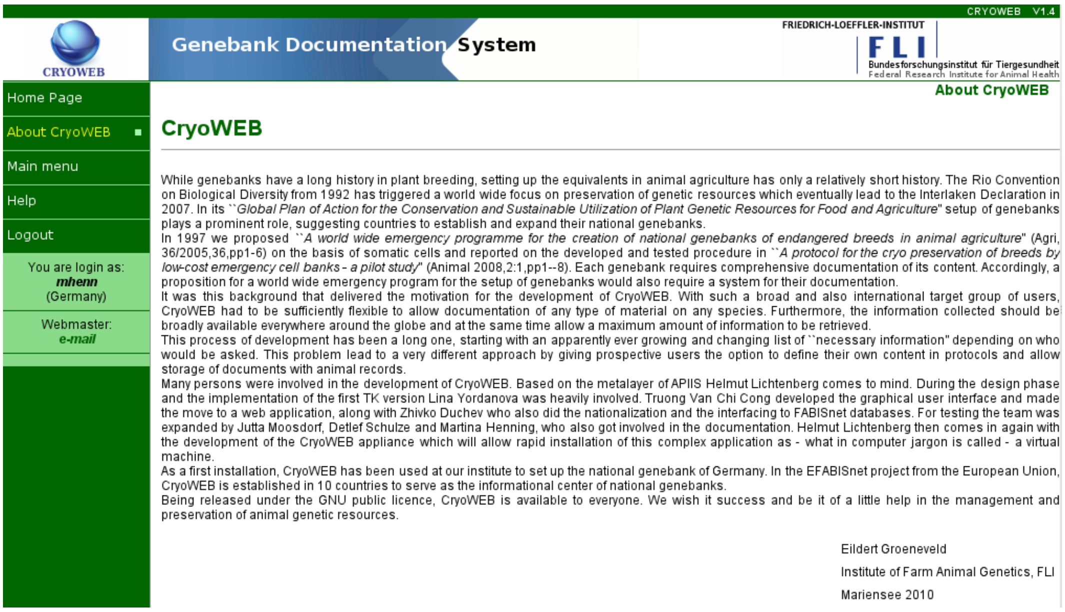
Home page - returns you to the initial page with the label CryoWEB.

About Cryo - this page (Figure 2.3) contains information about the history of Cryo-WEB, the motivation for this system, how it was designed, the people behind it, etc.

Main menu - this is the entry point to the main part of the page: the data management and reporting part. This item will be described in detail in the next chapter.

Help - in this page (Figure 2.4) the user is introduced to the various CryoWEB documentation and help options - the user manual, screen and field context help, and FAQ. The description of each help item includes also instructions for accessing it, and examples. Further, the page contains a link, where the user can download the current version of the User Manual.

Logout - exits the CryoWEB page and shows the initial login screen.



CryoWEB

While genebanks have a long history in plant breeding, setting up the equivalents in animal agriculture has only a relatively short history. The Rio Convention on Biological Diversity from 1992 has triggered a world wide focus on preservation of genetic resources which eventually lead to the Interlaken Declaration in 2007. In its ``*Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture*" setup of genebanks plays a prominent role, suggesting countries to establish and expand their national genebanks.

In 1997 we proposed ``*A world wide emergency programme for the creation of national genebanks of endangered breeds in animal agriculture*" (Agri, 36/2005,36,pp1-6) on the basis of somatic cells and reported on the developed and tested procedure in ``*A protocol for the cryo preservation of breeds by low-cost emergency cell banks - a pilot study*" (Animal 2008,2:1,pp1--8). Each genebank requires comprehensive documentation of its content. Accordingly, a proposition for a world wide emergency program for the setup of genebanks would also require a system for their documentation.

It was this background that delivered the motivation for the development of CryoWEB. With such a broad and also international target group of users, CryoWEB had to be sufficiently flexible to allow documentation of any type of material on any species. Furthermore, the information collected should be broadly available everywhere around the globe and at the same time allow a maximum amount of information to be retrieved.

This process of development has been a long one, starting with an apparently ever growing and changing list of ``necessary information" depending on who would be asked. This problem lead to a very different approach by giving prospective users the option to define their own content in protocols and allow storage of documents with animal records.

Many persons were involved in the development of CryoWEB. Based on the metalayer of APIIS Helmut Lichtenberg comes to mind. During the design phase and the implementation of the first TK version Lina Yordanova was heavily involved. Truong Van Chi Cong developed the graphical user interface and made the move to a web application, along with Zhivko Duchev who also did the nationalization and the interfacing to FABISnet databases. For testing the team was expanded by Jutta Moosdorf, Detlef Schulze and Martina Henning, who also got involved in the documentation. Helmut Lichtenberg then comes in again with the development of the CryoWEB appliance which will allow rapid installation of this complex application as - what in computer jargon is called - a virtual machine.

As a first installation, CryoWEB has been used at our institute to set up the national genebank of Germany. In the EFABISnet project from the European Union, CryoWEB is established in 10 countries to serve as the informational center of national genebanks.

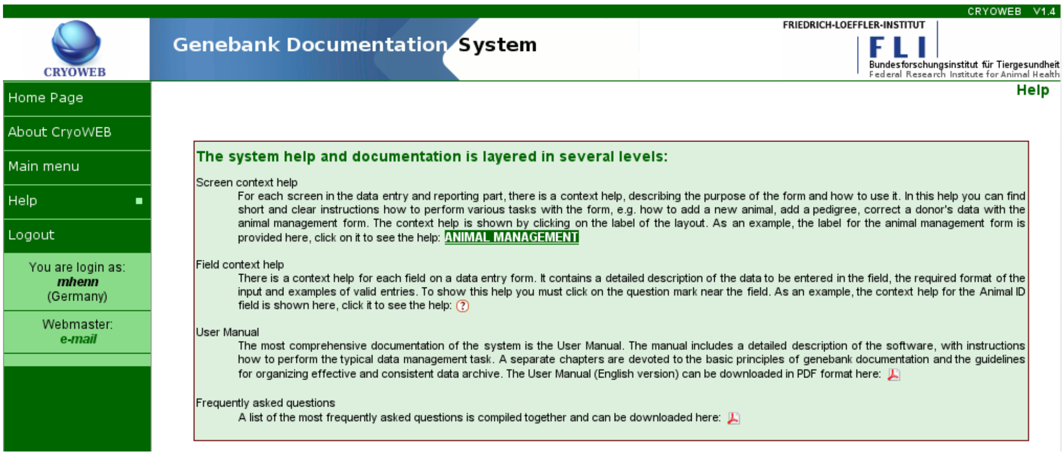
Being released under the GNU public licence, CryoWEB is available to everyone. We wish it success and be it of a little help in the management and preservation of animal genetic resources.

Eildert Groeneveld

Institute of Farm Animal Genetics, FLI

Mariensee 2010

Figure 2.3: About Cryo - short history and motivation of CryoWEB



The system help and documentation is layered in several levels:

Screen context help

For each screen in the data entry and reporting part, there is a context help, describing the purpose of the form and how to use it. In this help you can find short and clear instructions how to perform various tasks with the form, e.g. how to add a new animal, add a pedigree, correct a donor's data with the animal management form. The context help is shown by clicking on the label of the layout. As an example, the label for the animal management form is provided here, click on it to see the help: ANIMAL MANAGEMENT

Field context help

There is a context help for each field on a data entry form. It contains a detailed description of the data to be entered in the field, the required format of the input and examples of valid entries. To show this help you must click on the question mark near the field. As an example, the context help for the Animal ID field is shown here, click it to see the help: ?

User Manual

The most comprehensive documentation of the system is the User Manual. The manual includes a detailed description of the software, with instructions how to perform the typical data management task. A separate chapters are devoted to the basic principles of genebank documentation and the guidelines for organizing effective and consistent data archive. The User Manual (English version) can be downloaded in PDF format here:

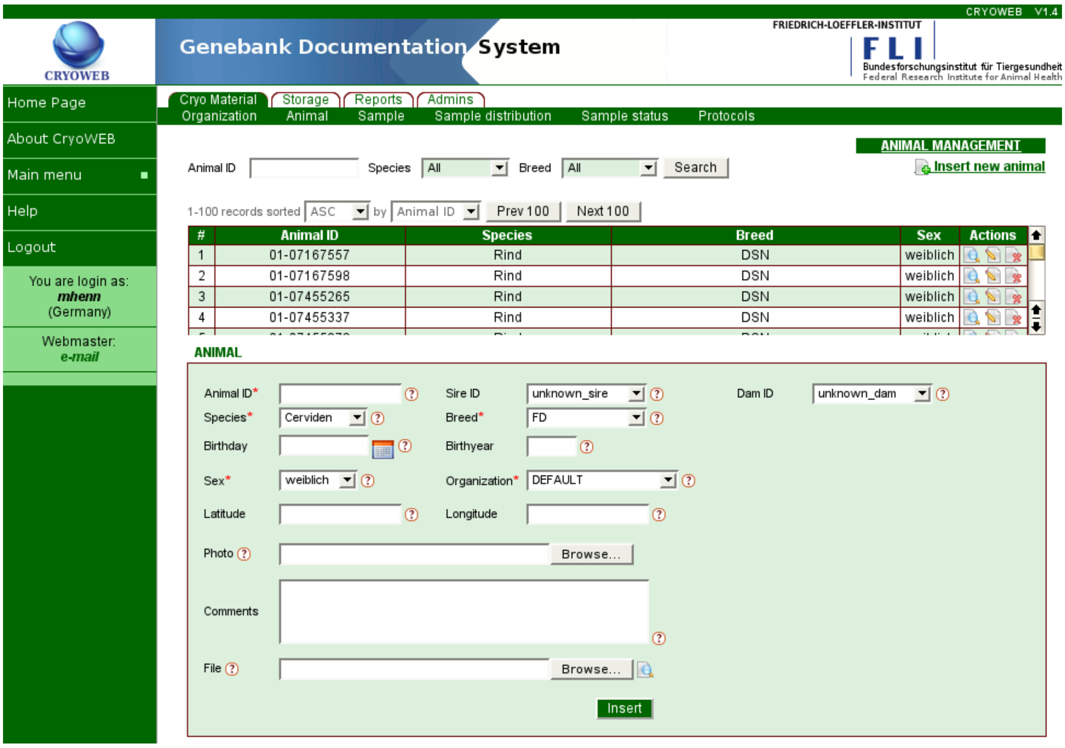
Frequently asked questions

A list of the most frequently asked questions is compiled together and can be downloaded here:

Figure 2.4: Help options- User Manual, context help, FAQ

2.3 Main menu

Clicking on the **Main menu** item opens the data management part of CryoWEB in the main area (Figure 2.5). On the top of the area is the two-level navigation menu bar and below it the data entry forms are placed. The first level in the menu contains four tabs - **Cryo Material**, **Storage**, **Reports** and **Admins**. When you click on one of these tabs, a group of sub-tabs is shown in the second level of the menu bar. Each sub-tab is linked to one web form, and clicking on one of the sub-tabs will show the respective form in the main area of the web page. For each tab of the menu a default sub-tab is set, thus clicking on the tab will show also the default sub-tab form on the screen.



Animal ID Species All Breed All

1-100 records sorted ASC by Animal ID

#	Animal ID	Species	Breed	Sex	Actions
1	01-07167557	Rind	DSN	weiblich	
2	01-07167598	Rind	DSN	weiblich	
3	01-07455265	Rind	DSN	weiblich	
4	01-07455337	Rind	DSN	weiblich	

Animal ID*
Sire ID: unknown_sire
Dam ID: unknown_dam
Species*: Cerviden
Breed*: FD
Birthday
Birthyear
Sex*: weiblich
Organization*: DEFAULT
Latitude
Longitude
Photo
Comments
File

Figure 2.5: The main data entry area with opened Animal form

> **Note:** On each menu click, CryoWEB connects to the server to generate the form with the last data available at the moment. Depending on the speed of your Internet connection, it may take some time before the form is shown and filled with data.

2.3.1 Cryo Material tab

Figure 2.6: The Cryo Material tab

The **Cryo Material** tab (Figure 2.6) consists of six sub-tabs. These are:

Organization - this form is used for recording the contact data for organizations and persons. It is intended for management of a contacts folder for all partners involved with the genebank. Here the organization name and contact person, address, phone and fax numbers, email and other data are recorded. All fields, except the organization identifier, are optional, i.e. the user could only fill in fields relevant to the organization under consideration.

Animal - this form is used for recording the basic data for the donors and their pedigree. Here the user should enter the unique identification for the donor, its breed and species and organization where more data for this animal can be obtained. Additionally, the geographic location of the donor, its image, birth date and documents, like birth certificate, can be added. Pedigree data is not mandatory, but pedigree of any length up to base animals can be entered. In case pedigree data is entered, each member of the donor's pedigree should be entered as a separate animal using the same form.

Sample - this form is used for entering data of new samples. Here the user registers the new unique sample identifier, the animal donor, the production, freezing and storage date, the type of packaging and protocol used along with the initial distribution of the sample in the storage (one sample may consist of many straws (i.e. units), in the case of semen). With this form the user can also correct sample data in case of errors.

Sample distribution - this form is used for managing the distribution of samples in the storage facilities. Here the user can correct the initial distribution entered via the **Sample** form, e.g. update the number of stored units, or add another location where sample units are stored.

Sample status - this form is used when the user wants to change the legal status of part of the sample units. Via this form only, the status for all units in a single cell can be changed (because of the system rule that in one cell all the units from a sample have to have the same status).

Protocols - this form is used for management of the protocols data for the sample, which are supposed to describe the collection and freezing procedure, along with guidelines for the thawing procedure to be followed. The exhaustive description should be stored in a file in a standard format, and this file must be uploaded along with the material type via the **Protocols** form.

The default sub-tab on the **Cryo Material** tab is **Organization**.

2.3.2 Storage tab

Figure 2.7: The Storage tab

The **Storage** tab (Figure 2.7) consists of five sub-tabs. These are:

Move Samples - this form is used to move part of a sample to another location within the genebank, or remove part of a sample from the genebank, e.g. use a straw for research. A movement of sample's units to another location is only allowed to cells containing units from this sample with the same status, or cells where no units from this sample are present.

Move Containers - via this form the user can record the moving of entire containers with their content to another location in the genebank. This can be moving of a tank (with all canisters intact) to different building or storage place, moving a canister into another tank, etc..

Browse Storage - this form is used for virtual navigation through the storage location hierarchy and viewing the samples stored in the single cells, i.e. for visualization of the content of the storage facilities. For a chosen sample in any cell, the user is presented with its complete distribution in the facilities, i.e. a list of all storage places where units from this sample are kept.

Manage Storage - this form is used for adding, renaming and removing elements in the locations hierarchy. This includes adding a new tank, re-labeling (renaming) canister, deleting a compartment, etc. The deletion of an element in the hierarchy leads to automatic deletion of all sub-levels, i.e. if the user deletes a tank, all canisters in this tank will be also deleted. Only empty containers can be deleted.

Overview - this form lists all the actions for a single sample, and allows the user to revert the last action. For example the user can revert the last movement of the sample units to another location.

The default sub-tab on the **Storage** tab is **Move Samples**.

2.3.3 Reports tab

Figure 2.8: The Reports tab

The **Reports** tab (Figure 2.8) consists of six sub-tabs. These are:

Animal Samples - via this form the user can create a report, listing all samples from a single animal donor. The form allows searching for the donor by its identification, identification of a sample from this donor, material type, production date, storage or any combination from these criteria. The report includes the general donor data - species, breed, pedigree, sex, organization, birth date, geographic location, and a list of all samples produced by that donor. For each sample its identification, production date, distribution in storage and status are included.

Genebank Statistics - on this form four reports can be created. The first one is named also **Genebank Statistics** and contains the total number of donors, samples and units per material type and breed. In this report, aggregation of the samples count is made also on the species level.
The second report is the **Samples List**. In this report a complete list of samples per breed and species is generated. For each sample its identification, material type, location, number of stored units in this location, and their status are listed. This report can be generated in two forms - **by location** or **by breed**. The former form is used for inventory purposes - to check the storage facilities. The latter is user for controlling the amount and location of the conserved material from a single breed, i.e. from conservation program perspective.
The third report - **Sires** lists for each breed the total number of male donors and the minimum, maximum and average number of units from males samples counted per material type.
The fourth report - **Dams** lists for each breed the total number of female donors and the minimum, maximum and average number of units from females samples counted per material type.
For each of these reports the additional filtering paramaters **storage place** and **breed** can be set prior to generation, e.g. the general genebank statistics can be generated only for a single location.

Search Offspring - this form is used to check the representation of a sire's or dam's offspring in the genebank. The search is done by animal identification (of the sire/dam). The resulting list contains the identifications of the donors and other animals which are offspring from that sire/dam including further details about the offspring.

Movements - this report lists all movements of sample units within the genebank and the release of germplasm out of the genebank for a given period. The changes in samples status are also listed here. The report can be further filtered by location, i.e. only movements from and to a chosen storage are listed.

Sample Movements - this report lists, in chronological order, all movements and status changes of a single sample. The sample can be found by its identification number, by the identification of the donor, by the material type, production date, or a combination of the above.

Animals distribution - this form produces a file for graphical visualization of the geographical distribution of the donor animals from a single breed. The prerequisite for such report is the recording of the donors location on the animal form. The user has to choose species and breed and export the data. In CryoWEB the positioning of the donors is done on the maps provided by **Open Street Map**, but if you need more sophisticated maps you can use the exported KML file and opened it in the **Google Earth** software, or in **Google Maps**. There, the location of the donors along with the total amount of conserved material by donor is shown.

The default sub-tab on the **Reports** tab is **Animal Samples**.

2.3.4 Admins tab

Figure 2.9: The Admins tab

The **Admins** tab (Figure 2.9) consists of three sub-tabs. These are:

Codes - here the CryoWEB administrator can manage content of the drop-down lists to be used on the data entry and report forms. This includes the adding of species and breeds names, vessel types, legal status values.

Link breeds - as the same breed name may be used in different species, the administrator needs to link each breed name to be used in CryoWEB to one or more species. This is done on the Link breeds form.
There is also second type of linking to be done on the same form. If accumulated data per breed has to be exported for EFABIS (see next item), the breed and species names used in CryoWEB must be linked to the respective breed and species names in EFABIS.

EFABIS export - This is a special feature for the national coordinators for management of animal genetic resource, who want to use CryoWEB as data source for the European Farm Animal Biodiversity Information System. In this system, aggregated per year, population and material type, conservation statistics are collected. The data required by EFABIS is the amount of cryo-conserved material per breed which can be exported via this form.

The default sub-tab on the **Admins** tab is **Codes**.

Figure 2.10: Icons on a data entry form

2.4 General data entry form

The data entry form has a uniform layout, which is followed by most forms in CryoWEB. The form/layout name is positioned in the upper right part of the form. This name is also a hyperlink to online help for the layout. In the upper left part of the form is the search area, where the user can specify a number of search criteria. The results from the search are listed in the table below the search area. Its first column is used for numbering the results, the last column contains the actions while the in between columns present the data returned from the query.

The results can be ordered ascending or descending by one of the columns; the sorting controls are located just above the results table. When the user changes the sorting order, the search is executed again with the current values in the search area, thus the results may differ. Even with the same search criteria the results may be different as the data is read again from the database, and in the meantime it may have been updated by another user.

The results are shown in groups of 100 lines which can be advanced by the navigation buttons to the next (previous) 100 lines, which are located between the search area and the results table. The navigation to the next/previous 100 records also reads the actual data from the database, thus the results may differ if the database has been updated in the meantime.

The actions in the last column of the results table are the **View**, **Update** and **Delete**. Clicking on one of these icons in a record line fills the data entry form in the lower part of the screen with the detailed data from the chosen record. At the same time the action of the form is set to **View**, **Update** and **Delete** and the label of the submit button is changed respectively. The **View** action is intended to show the details of the chosen record, preventing the user from unwanted modifications. The **Update** action is used for corrections in data. The **Delete** action is used for deletion of records, usually when these records are not referred by others. In any case the record details are also shown in the form for the user to check, if this is indeed the intended record for deletion. Two other special actions are used on the **Move Samples** form for the **Move** and **Remove** actions. The standard action on the **Reports** forms is **Export to Pdf**. The icons for all described actions are shown in Figure 2.10.

The general workflow for modifying data starts with searching the record to be modified, using a combination of the search criteria. The user should then navigate through the results list, until the line with the record is shown on the screen, and click the icon of the respective action in that line. The data should then be updated in the data entry part, and in order to send the changes to the database the submit button must be clicked.

The insertion of a new record is separated from the other actions, both, logically and visually. The **Insert** action icon and link is positioned in the upper right part of the form just below the layout name. After clicking on the insert icon, the submit button of the data entry form changes to **Insert**. On some forms clicking of the **Insert** action presets part of the field values, e.g., the **Material type** on the **Protocols** form is preset from the selection in the search part.

After the user submits the form, the data is sent to the database. If the action is successfully executed, a short notification is shown for five seconds in the lower left part of the main area on the page. This message reads **<Action>: Action successfully executed**, e.g.

```
Update: Action successfully executed
```

In case of errors, a pop-up window will be shown with the error message and the erroneous field will be highlighted in red.

3 Installation of CryoWEB

3.1 Introduction

CryoWEB is a Web application accessible through the network. Such a Web server consists of a complete operating system, the actual web server like Apache, the database system, many system software components and finally the CryoWEB application software. All of these individual components need to be correctly configured to operate smoothly. Building a system like this from individual components is a daunting task, which many potential users will find overwhelming.

With the development of virtualization in computing, so called appliances open up a whole new way of installing complex software systems. An appliance presents itself to the prospective user as one big data file, that may be a few hundred MB in size. It can be thought of as a copy of a hard disk, that holds the complete operating system installation plus all other software required for a fully functioning computer, i.e. it is a virtual computer. The beauty of a virtual computer is, that it can be transferred to another already existing computer, and then be started on that computer as a guest system. To the outside world it looks just the same as a new hardware computer with all the features of a separate box. A further advantage is that the host operating system and the operating system in the appliance (i.e. the guest system) can be different. The CryoWEB appliance is a complete Linux system. Copied to a Windows system as a host, it will start a complete Linux system as a guest without the user having to configure the guest system: it is already completely configured, everything is contained in that appliance file.

While the host system itself is complete and fully configured, its connection to the network is of course not. And this is the part, that will be described now.

3.2 Getting the appliance

The CryoWEB appliance can be downloaded from the ftp-server of the Institute of Farm Animal Genetics (FLI). There are two directories:

`ftp://ftp.tzv.fal.de/pub/cryoweb/doc/`

and

`ftp://ftp.tzv.fal.de/pub/cryoweb/appliance/`

The doc-subdirectory contains this CryoWEB **User Guide**, whilst the appliance subdirectory contains the software. Download the latest versions with:

`ftp://ftp.tzv.fal.de/pub/cryoweb/appliance/current-vmware.zip for VMWare Player`

`ftp://ftp.tzv.fal.de/pub/cryoweb/appliance/current-virtualbox.zip for VirtualBox`

and

`ftp://ftp.tzv.fal.de/pub/cryoweb/doc/cryoweb_manual.pdf`

This zip-archive at `ftp://ftp.tzv.fal.de/pub/cryoweb/appliance/current-vmware.zip` is about 800 MB in size and contains three files:

- `cryoweb.vmdk`, the virtual computer in one big file. Unpacked it takes about 2 GB of disk space. During use it can grow up to 14 GB, depending mainly on the size of your database.
- `cryoweb.vmx`, a small file of less than 2 KB, containing the configuration for the appliance
- `INSTALL-cryoweb`, also around 2 KB of size with short instructions, how to install the CryoWEB appliance for VMWare Player

3.3 Host system requirements

As has been stated above, an appliance contains all of the software of a standalone computer system. Being a 'virtual' computer, it runs as a guest on top of an already existing system, the host. This implies that both systems, the host and the guest need to share the one existing hardware. Components to consider are the CPU, the RAM, and the disk.

As already mentioned before, the appliance comes as one large file which in its uncompressed form takes up about 2GB. The maximum size is allowed to grow to 14GB: the appliance starts growing as more data get entered. Even if the amount of numerical data may not go into millions for a medium size lab, adding images and archives containing image data may expand the database considerably. However, given the increase in disk sizes and reduced prices for sufficient disk space, this is not really an issue any more. It may make sense to put the appliance on a separate partition or even disk. One aspect to consider is backup. Database dumps should be generated at regular intervals. As they are copies of the database, also the disk requirement at that event will double. Generally speaking, anything above 20GB disk space should be fine.

As with disk space also the prices for memory or RAM have drastically gone down. While additional disk space for an appliance will often be available, the situation may be different for RAM. Here, the memory installed is usually matched to the jobs to be run on that computer. Thus, adding one “computer” as an appliance requires RAM to be allocated and, thus, taken away from the host. It seems that CryoWEB and its complete operating system runs happily in 1GB. So with a total of 2GB of RAM in the computer, which is intended to serve as a host, you should be on the safe side.

When available, appliances use special hardware virtualization feature, called “Hardware Assisted Virtualization” which, both, current Intel and AMD processors should support. Thus, check for AMD-V and Intel VT-x for the CPU on the intended host machine. Without this feature, the appliance may run, but it will be impracticably slow.

The appliances will run on a 32bit and 64bit CPU, so no special considerations are required here. However, if you have the choice, a multicore CPU should be preferred. With this, the normal interactive operations on the host machine will continue as before, as the guest will most likely be executed on the other CPU cores.

This leads to the final question: what type of computer is required in terms of desktop or server system? From systematics point of view, the appliance should run on a server, because it *is* a server, a Web server to be more precise. This means that requests external to the appliance will get directed at it (through cryobank people pointing their browser at the CryoWEB Web server). Such requests will of course only get honored, if the Web server is up and running. Now servers are usually kept running around the clock, and are located in separate rooms not accessible to everyone. This would also be the preferred environment for CryoWEB.

On the other hand, technically, the CryoWEB appliance will run on any modern desktop hardware. At the time of this writing, desktop machines with 1TB of disk space, 4GB of RAM and a multicore CPU are being offered at €500, and are more than sufficient to serve as a host.

One last requirement should be self evident: if CryoWEB is to be accessed from any browser on the network, the physical host computer needs to be connected to the network, requiring an Ethernet card and the corresponding cable connection. There is only one situation, where this may not be required: If CryoWEB is to be used on one computer only, the Web browser of the host would be sufficient. Then, no network connection outside the host system is required. Instead, the host and the guest would be the only two ’computers’ in the network.

3.4 Installing the appliance

As stated above, an appliance is a virtual computer, that runs on another computer (the so called host) without touching the host’s installation. The appliance is driven by some virtualization software, which has to be installed before. Here we will present two of the options freely available - the VMWare Player and VirtualBox. To cover also the various operating systems, the installation with VMWare Player will be described under MS Windows OS, and the installation with VirtualBox in GNU

Linux OS. However, this does not mean that we are giving preference to a certain software in a certain OS.

3.4.1 Installation with VMWare Player

The VMWare Player is provided by a company called VMware, Inc. Download the VMWare Player software specifically for your host operating system from:

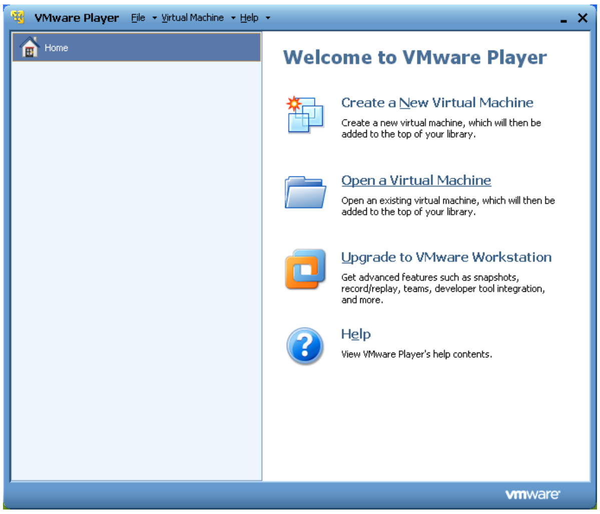
http://www.vmware.com

Installation of VMWare Player is straight forward when you follow the instruction on the web page.

After you have installed it successfully, create a directory (e.g. C:\vmware\CryoWEB) to put the appliance into. Unpack the downloaded zip-file with the appliance here, resulting in three files:

1. `C:\vmware\cryoweb\cryoweb.vmdk`
2. `C:\vmware\cryoweb\cryoweb.vmx`
3. `C:\vmware\cryoweb\INSTALL-cryoweb`

Now all prerequisites are in place and you can start VMWare Player. The initial window of the application is shown in Figure 3.1.



Welcome to VMware Player

Create a New Virtual Machine

Create a new virtual machine, which will then be added to the top of your library.

Open a Virtual Machine

Open an existing virtual machine, which will then be added to the top of your library.

Upgrade to VMware Workstation

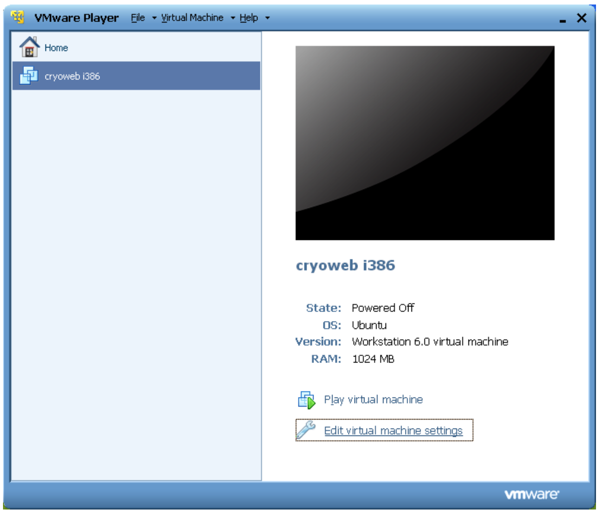
Get advanced features such as snapshots, record/replay, teams, developer tool integration, and more.

Help

View VMware Player's help contents.

Figure 3.1: Opening a new appliance

In the VMWare Player click on **Open a Virtual Machine** to the right (see Figure 3.1) to open a file selection window, and choose `there C:\vmware\cryoweb\cryoweb` (or your appropriate path to the CryoWEB appliance). The appliance will then be listed in the left column of the player (Figure 3.2).



cryoweb i386

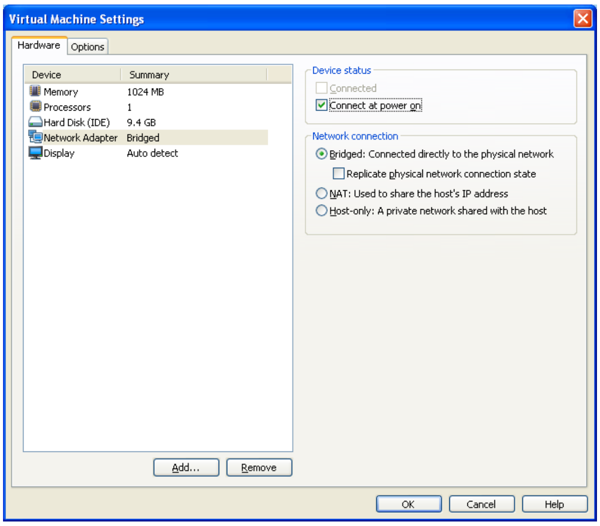
State: Powered Off
OS: Ubuntu
Version: Workstation 6.0 virtual machine
RAM: 1024 MB

Figure 3.2: Tuning the new appliance

The link **Edit virtual machine settings** (see Figure 3.2) leads you to a configuration window with two tabs - **Hardware** and **Options**. Via the options on the **Hardware** tab you can control the virtual hardware of your appliance - the amount of memory allocated to the appliance, the hard disk space, the type of the network connection and display settings. The **Options** tab allows you to control the appliance name, guest operating system and working folder, to set shared folders for data exchange between the host and the guest, configure notifications for the VMWare Tools, etc..

In the **Hardware** configuration window (Figure 3.3), you should adapt the memory settings, according to the installed memory in your host computer. It is recommended to have 2GB RAM in your host as you will run two operating systems and a lot of auxiliary programs like the VMWare Player and the database and web server in the appliance.

The network settings depend on your local setup. If in doubt, contact your network administrator. The default setting for the appliance is to poll a DHCP-Server for the necessary information like IP-Address, network mask, or DNS name server. You will find the MAC-Address of the appliance (needed for configuring your DHCP-Server) in the file C:\vmware\cryoweb\INSTALL-cryoweb.



Device	Summary
Memory	1024 MB
Processors	1
Hard Disk (IDE)	9.4 GB
Network Adapter	Bridged
Display	Auto detect

Device status

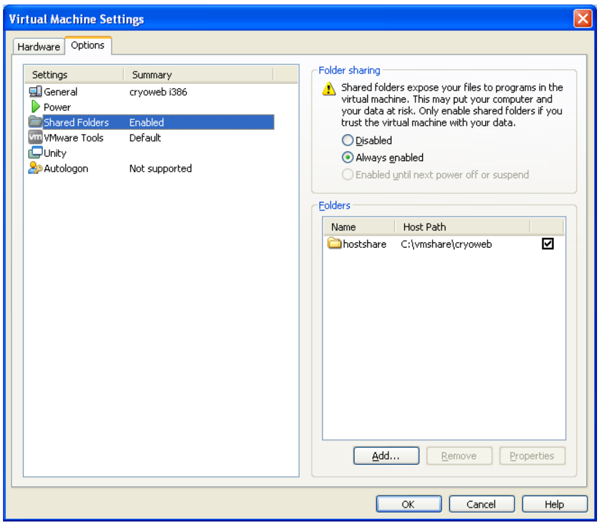
☐ Connected
☑ Connect at power on

Network connection

● Bridged: Connected directly to the physical network
☐ Replicate physical network connection state
○ NAT: Used to share the host's IP address
○ Host-only: A private network shared with the host

Figure 3.3: Configuring the hardware

In the **Options** tab (Figure 3.4), the **Shared Folders** item is of main interest.



Settings	Summary
General	cryoweb i386
Power	
Shared Folders	Enabled
VMware Tools	Default
Unity	
Autologon	Not supported

Folder sharing

Shared folders expose your files to programs in the virtual machine. This may put your computer and your data at risk. Only enable shared folders if you trust the virtual machine with your data.

○ Disabled
● Always enabled
○ Enabled until next power off or suspend

Folders

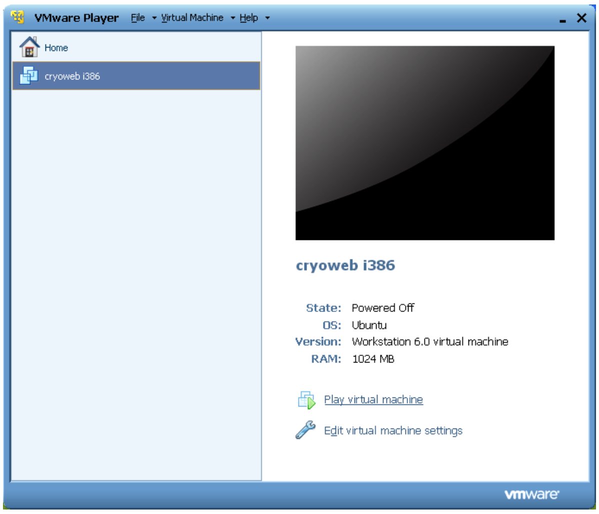
Name	Host Path	
hostshare	C:\vmshare\cryoweb	☑

Figure 3.4: Other configuration options

This enables data exchange between the appliance and the host. By default, a folder `C:\vmshare\cryoweb` is shared with a directory within the appliance. You have to create the C:\vmshare\cryoweb folder in you host system (MS Windows), or change this setting, if it does not fit into your local setup and point it to existing folder on your hard disk. Please do not change the name *hostshare*, as this points to a folder with this same name inside the appliance. When you change it, you will be unable to use the dump/restore via the vmadmin account.

This shared folder is used to backup (dump) the CryoWEB-database and gives you also a convenient way to restore your database. The same folder is used also for the transfer of the localization files between the appliance and the host machine.

Now you can power up your virtual machine by clicking **Play virtual machine** as shown in Figure 3.5.



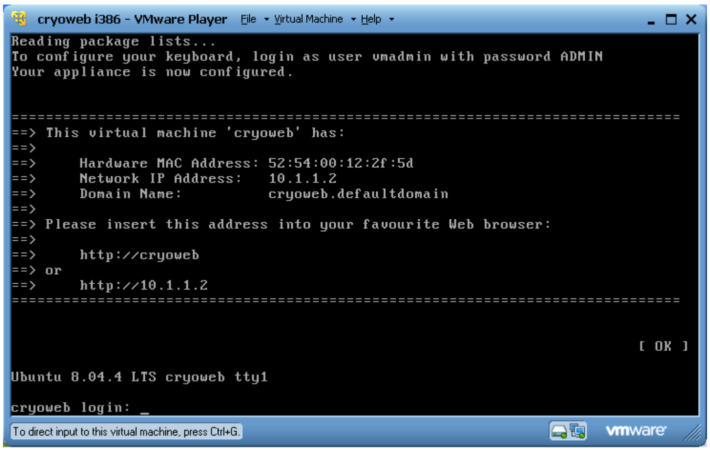
cryoweb i386

State: Powered Off
OS: Ubuntu
Version: Workstation 6.0 virtual machine
RAM: 1024 MB

Figure 3.5: Powering on the appliance

The appliance boots like a normal computer in the VMWare Player window. At the end of the boot process, some basic information about your network settings are displayed (Figure 3.6). Very important here is the **Network IP Address**. If there is no value in that line, then the appliance has failed in obtaining a valid IP address. As a result, the users will not be able to access the CryoWEB web page. In such case verify, together with the local network administrator, the network settings in the **Hardware** tab.

If you want to run more than one CryoWEB appliance in your network, keep in mind that all CryoWEB appliances have by default the same MAC-Address. To change the MAC-Address of the appliance you have to edit directly the `cryoweb.vmx` file using a text editor.



```
Reading package lists...
To configure your keyboard, login as user vmadmin with password ADMIN
Your appliance is now configured.


==============================================================================
==> This virtual machine 'cryoweb' has:
==>
==>     Hardware MAC Address: 52:54:00:12:2f:5d
==>     Network IP Address:   10.1.1.2
==>     Domain Name:          cryoweb.defaultdomain
==>
==> Please insert this address into your favourite Web browser:
==>
==>     http://cryoweb
==> or
==>     http://10.1.1.2
==============================================================================


                                                                        [ OK ]

Ubuntu 8.04.4 LTS cryoweb tty1

cryoweb login: _
```

To direct input to this virtual machine, press Ctrl+G.

Figure 3.6: Freshly booted VMWare appliance

The log in prompt shown here *cryoweb login:* should only be used for administrative tasks.

3.4.2 Installation with VirtualBox

The VirtualBox software from Oracle comes in two free editions - Open Source Edition (OSE) released under GPL and binary form for personal use and evaluation under PUEL license. The PUEL edition can be downloaded specifically for your host operating system from:

http://www.virtualbox.org/wiki/Downloads

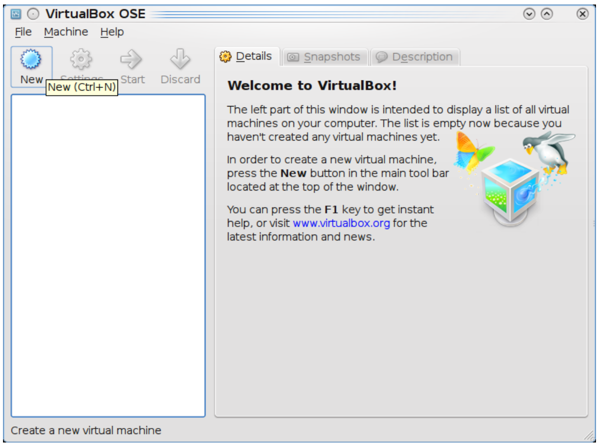
The OSE edition is available as package in many of the Linux distributions, so get it via your favourite setup and configuration tool, like Aptitude, Yast, etc. In the text below we will use the VirtualBox OSE under Ubuntu 9.10.

After you have installed VirtualBox successfully, create a directory (e.g. ~/vmware/cryoweb) to put the appliance into. Unpack from the current-virtualbox.zip file the virtual machine disk:

1. `cryoweb.vmdk`

You have to create a new virtual machine in VirtualBox. Further, you need to create a folder on your host machine which will be used for exchanging data between the host and the appliance, e.g. where the database will be dumped. By default this folder is /data, so you have to create it on your machine and set read/write permissions at least to yourself. Now all prerequisites are in place and you can start VirtualBox.

Click on **New** button to create a new virtual machine (Figure 3.7)



Welcome to VirtualBox!

The left part of this window is intended to display a list of all virtual machines on your computer. The list is empty now because you haven't created any virtual machines yet.

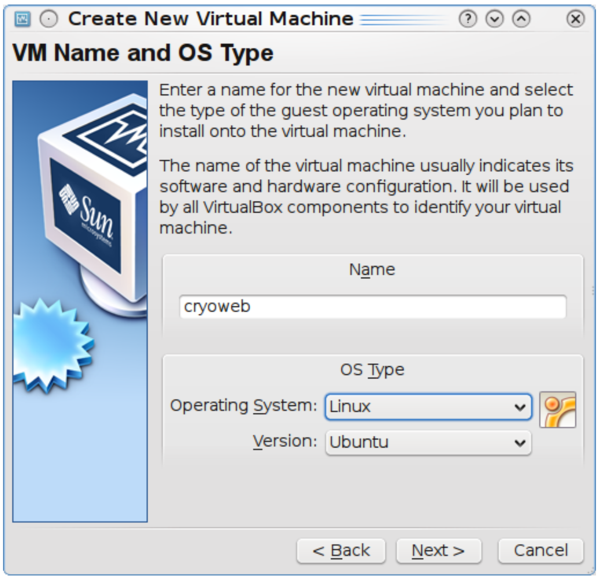
In order to create a new virtual machine, press the **New** button in the main tool bar located at the top of the window.

You can press the **F1** key to get instant help, or visit www.virtualbox.org for the latest information and news.

Create a new virtual machine

Figure 3.7: Creating a new appliance in VirtualBox

Click **Next** button in the wizard to get to the **VM Name and OS type** screen (Figure 3.8), where you have to set the name of the new virtual machine.



Enter a name for the new virtual machine and select the type of the guest operating system you plan to install onto the virtual machine.

The name of the virtual machine usually indicates its software and hardware configuration. It will be used by all VirtualBox components to identify your virtual machine.

Name: cryoweb

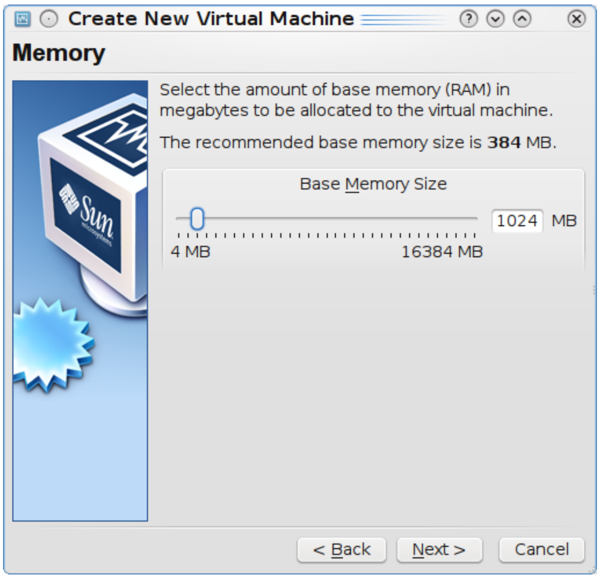
Operating System: Linux

Version: Ubuntu

Figure 3.8: Naming the new virtual machine

Enter **cryoweb** as the name for the new appliance. From the Operating System drop-down list choose **Linux**. From the Version drop-down list select **Ubuntu** as shown in Figure 3.8 (the guest operating system of the CryoWEB appliance is Ubuntu GNU/Linux). Then click **Next>** to continue.

On the next screen (Figure 3.9) you have to select the amount of memory to be allocated to your new virtual machine. This amount depends very much on the RAM you have on your machine, but it should not be less than 500 MB. It is advisable to set the amount of memory to at least 1 GB. If your genebank information system will be simultaneous accessed by many users then also the amount of allocated memory (and the physical RAM respectively) should be increased.



Select the amount of base memory (RAM) in megabytes to be allocated to the virtual machine.

The recommended base memory size is **384** MB.

Base Memory Size: 1024 MB

Figure 3.9: Allocating memory to the new virtual machine

After you set the slider control to the desired value click **Next>** to continue to the next screen in the sequence.

On the next screen you have to attach a hard disk to your appliance. Here, you will use the virtual machine disk you have extracted from the zip file. Make sure that the **Boot Hard Disk (Primary Master)** option is checked. Then choose the **Use existing hard disk** option (Figure 3.10) and click the folder icon to the right of the drop-down list.

Virtual Hard Disk

Select a hard disk image to be used as the boot hard disk of the virtual machine. You can either create a new hard disk using the **New** button or select an existing hard disk image from the drop-down list or by pressing the **Existing** button (to invoke the Virtual Media Manager dialog).

If you need a more complicated hard disk setup, you can also skip this step and attach hard disks later using the VM Settings dialog.

The recommended size of the boot hard disk is **8192** MB.

☑ Boot Hard Disk (Primary Master)

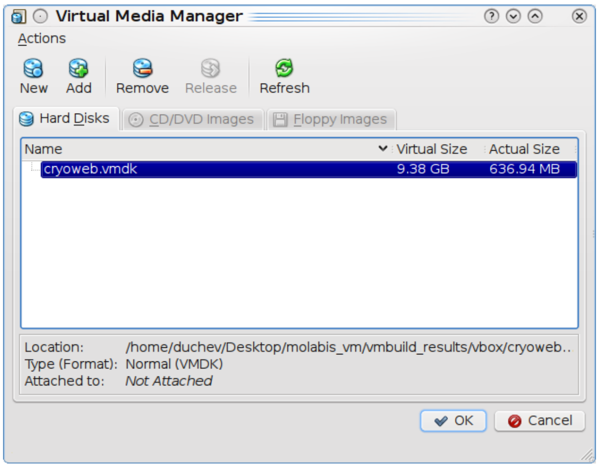
○ Create new hard disk

● Use existing hard disk

<no media>

Figure 3.10: Adding hard disk to the new virtual machine

A new form (**Virtual Media Manager**) will pop-up (Figure 3.11), where you can select the hard disk.



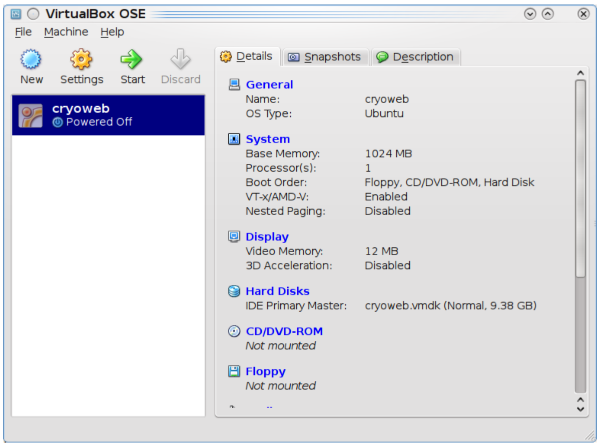
Name	Virtual Size	Actual Size
cryoweb.vmdk	9.38 GB	636.94 MB

Location: /home/duchev/Desktop/molabis_vm/vmbuild_results/vbox/cryoweb..
Type (Format): Normal (VMDK)
Attached to: *Not Attached*

Figure 3.11: Adding hard disk to the new virtual machine

If you do not see `cryoweb.vmdk` in the list of hard disks on this form, click on the **Add** button. In the pop-up file selection window navigate to the folder, where you have saved the `cryoweb.vmdk` and choose this file. The pop-up window will be closed and the `cryoweb.vmdk` file will be listed (and highlighted) in the **Hard Disks** list on the **Virtual Media Manager** form(as shown in Figure 3.11).

Click the **OK** button to close this form and return to the **Virtual Hard Disk** window. There click on the **Next>** button to go to the last screen in the wizard - the **Summary** screen, where you can control the configuration of the new virtual machine. Click the **Finish** button to create the new virtual machine in VirtualBox. The new machine is listed in the left column (Figure 3.12).



General
Name: cryoweb
OS Type: Ubuntu

System
Base Memory: 1024 MB
Processor(s): 1
Boot Order: Floppy, CD/DVD-ROM, Hard Disk
VT-x/AMD-V: Enabled
Nested Paging: Disabled

Display
Video Memory: 12 MB
3D Acceleration: Disabled

Hard Disks
IDE Primary Master: cryoweb.vmdk (Normal, 9.38 GB)

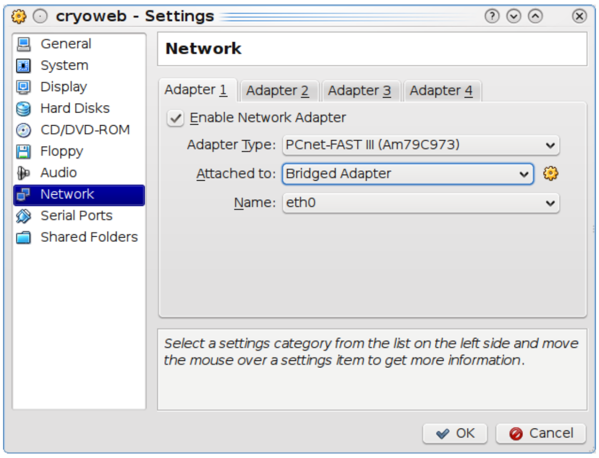
CD/DVD-ROM
Not mounted

Floppy
Not mounted

Figure 3.12: Changing the default settings in the new appliance

Now you have to change some of the default settings for the new appliance to match your network. The network settings depend on your local setup. If in doubt, contact your network administrator. The default setting for the appliance is to poll a DHCP-Server for the necessary information like IP-Address, network mask, or DNS name server.

Click on the **Settings** button and in the new window click on the **Network** icon in the left column (Figure 3.13). Choose from the **Attached to:** list the value **Bridged Adapter** and from the **Name** list choose your network card. If you have only one network card, it will be selected by default.



☑ Enable Network Adapter

Adapter Type: PCnet-FAST III (Am79C973)

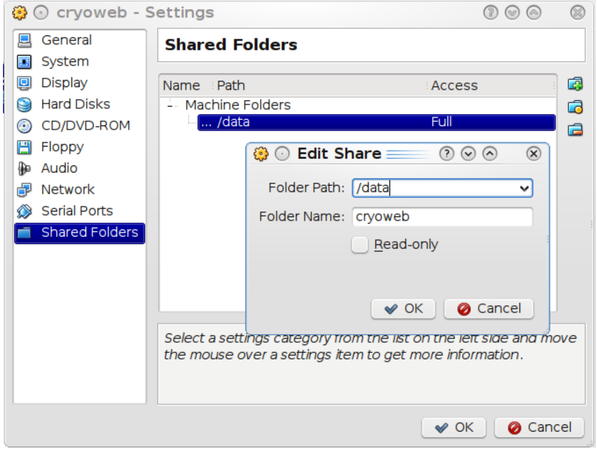
Attached to: Bridged Adapter

Name: eth0

Select a settings category from the list on the left side and move the mouse over a settings item to get more information.

Figure 3.13: Setting the network adapter

The next item to be set are the shared folders. Click on the **Shared Folders** item in the list on the left side (Figure 3.14), then click the **Add new shared folders** icon (the + icon) on the right.



Name	Path	Access
- Machine Folders		
	… /data	Full

Folder Path: /data

Folder Name: cryoweb

☐ Read-only

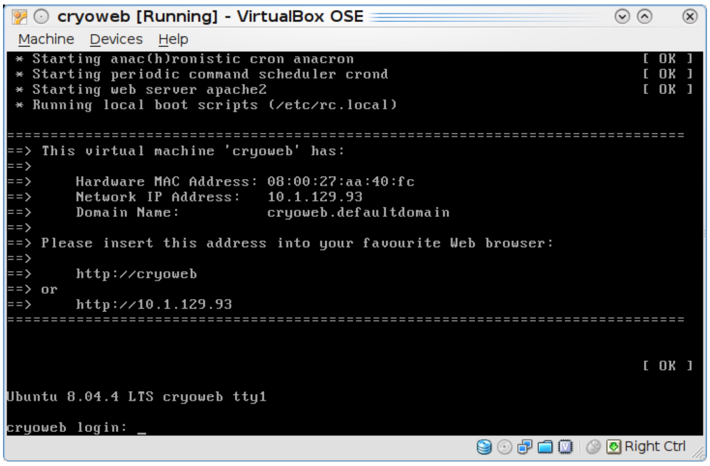
Select a settings category from the list on the left side and move the mouse over a settings item to get more information.

Figure 3.14: Setting the shared folders

In the pop-up window choose /data (or the folder you have chosen to share) for the **Folder Path** and **cryoweb** for **Folder Name**. Although the **Folder Path** on your machine may be different the **Folder Name** must stay always **cryoweb** as this name is used in the appliance.

Click **OK** on the **Edit Share** window, and then confirm all settings by clicking the **OK** button on the **Settings** window.

Now boot the appliance by clicking the **Start** button (see Figure 3.12).The appliance boots like a normal computer in the VirtualBox window. At the end of the boot process, some basic information about your network settings are displayed (Figure 3.15).



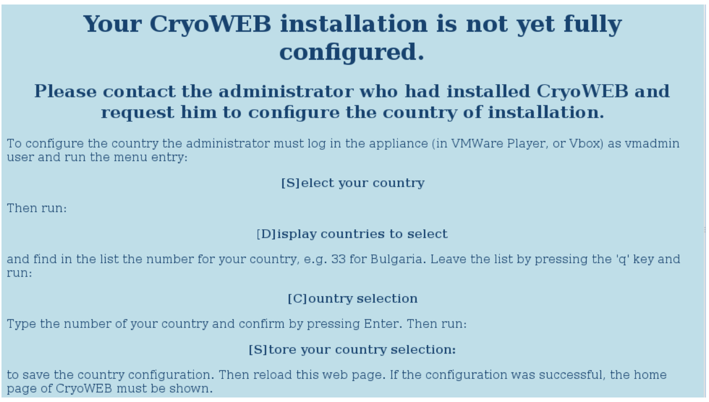
```
 * Starting anac(h)ronistic cron anacron                                  [ OK ]
 * Starting periodic command scheduler crond                              [ OK ]
 * Starting web server apache2                                            [ OK ]
 * Running local boot scripts (/etc/rc.local)

==============================================================================
==> This virtual machine 'cryoweb' has:
==>
==>     Hardware MAC Address: 08:00:27:aa:40:fc
==>     Network IP Address:   10.1.129.93
==>     Domain Name:          cryoweb.defaultdomain
==>
==> Please insert this address into your favourite Web browser:
==>
==>     http://cryoweb
==> or
==>     http://10.1.129.93
==============================================================================


                                                                          [ OK ]

Ubuntu 8.04.4 LTS cryoweb tty1

cryoweb login: _
```

Figure 3.15: Freshly booted VirtualBox appliance

3.4.3 Final settings for the installation

After you boot the appliance (either in VMWare Player or VirtualBox) you must set a country for the CryoWEB. This setting configures the installation for a single country. If, for example, you configure Austria as the country of installation, then all breeds entered via the web interface are considered coming from this country and will be exported as Austrian breeds in the yearly statistics file. If this setting is not done, the user will not be able to use the CryoWEB and will see instead the following page (Figure 3.16).

To configure the country follow the instructions from the screenshot (Figure 3.16), or the description of the country selection in Section 3.5. The selection of a country can be done only once, therefore be careful. In case of error, you must install again a new appliance, boot it and then set the country.



Your CryoWEB installation is not yet fully configured.

Please contact the administrator who had installed CryoWEB and request him to configure the country of installation.

To configure the country the administrator must log in the appliance (in VMWare Player, or Vbox) as vmadmin user and run the menu entry:

[S]elect your country

Then run:

[D]isplay countries to select

and find in the list the number for your country, e.g. 33 for Bulgaria. Leave the list by pressing the 'q' key and run:

[C]ountry selection

Type the number of your country and confirm by pressing Enter. Then run:

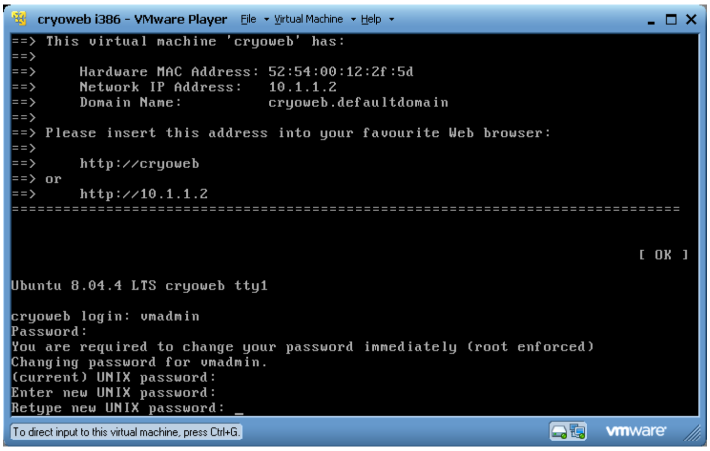
[S]tore your country selection:

to save the country configuration. Then reload this web page. If the configuration was successful, the home page of CryoWEB must be shown.

Figure 3.16: CryoWEB installation is not fully configured

3.5 Configuration options

The CryoWEB appliance is mainly an encapsulated complete service with the main interface via the CryoWEB webpage. Nevertheless there are a few settings, which would be nice to be adjustable, e.g. keyboard settings or backup. For tasks like those, the CryoWEB team provides a restricted administration interface, which hides the complexity of a whole operating system (Linux Ubuntu in this case) from the user.

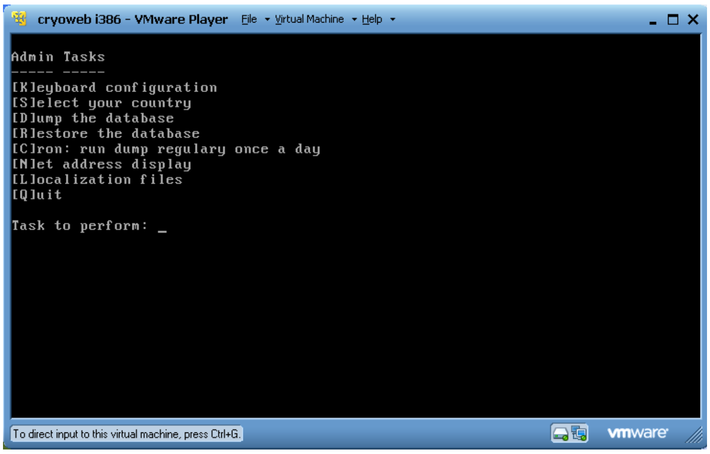


```
==> This virtual machine 'cryoweb' has:
==>
==>     Hardware MAC Address: 52:54:00:12:2f:5d
==>     Network IP Address:   10.1.1.2
==>     Domain Name:          cryoweb.defaultdomain
==>
==> Please insert this address into your favourite Web browser:
==>
==>     http://cryoweb
==> or
==>     http://10.1.1.2
=============================================================================

                                                                      [ OK ]

Ubuntu 8.04.4 LTS cryoweb tty1

cryoweb login: vmadmin
Password:
You are required to change your password immediately (root enforced)
Changing password for vmadmin.
(current) UNIX password:
Enter new UNIX password:
Retype new UNIX password: _
```

Figure 3.17: Logging in as vmadmin

When you look again at the appliance screen after the boot process (Figure 3.17), you can see a login prompt at the very bottom. A special user vmadmin (Virtual Machine Admin) leads you to the administration interface. Type vmadmin at the login prompt and hit Return. The first time you log in, the preset password is ADMIN (all in capital letters). Type in this password. Then this password is expired and you have to set another one. First you must repeat ADMIN at the prompt *(current) UNIX password:*. The new password must be typed in and retyped again.

The successful login provides you the administration interface (Figure 3.18).



```
Admin Tasks
----- -----
[K]eyboard configuration
[S]elect your country
[D]ump the database
[R]estore the database
[C]ron: run dump regulary once a day
[N]et address display
[L]ocalization files
[Q]uit

Task to perform: _
```

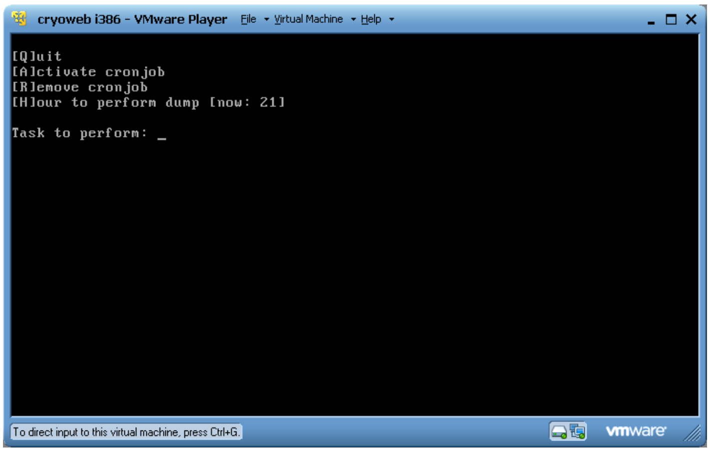
Figure 3.18: Administration interface

The *Keyboard configuration* option allows to configure the virtual machine according to the layout of your local keyboard. You need this only if you login directly at the login prompt in your VMWare Player or VirtualBox window. Just follow the screens and choose the appropriate values.

Dump the database writes a dump (backup) of your CryoWEB database data into the shared folder, e.g. C:\vmshare\cryoweb. The file name will be cryoweb_export.dump.

If you have to restore the database, maybe in case of a hard disk crash, you take your most recent dump file, rename it to cryoweb_import.dump and put it into your shared folder, for instance as `C:\vmshare\cryoweb\cryoweb_import.dump`. After you have done this, select the *Restore the database* option. The old database will be deleted, and the state from the dump file will be restored.

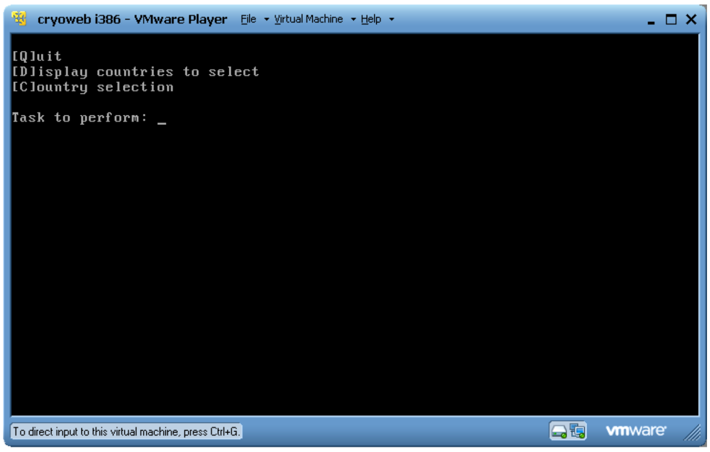
You can install an automatic, regular daily dump of your database by selecting *Cron: run dump regularly once a day*.



```
[Q]uit
[A]ctivate cronjob
[R]emove cronjob
[H]our to perform dump [now: 21]

Task to perform: _
```

Figure 3.19: Configure a regular database dump

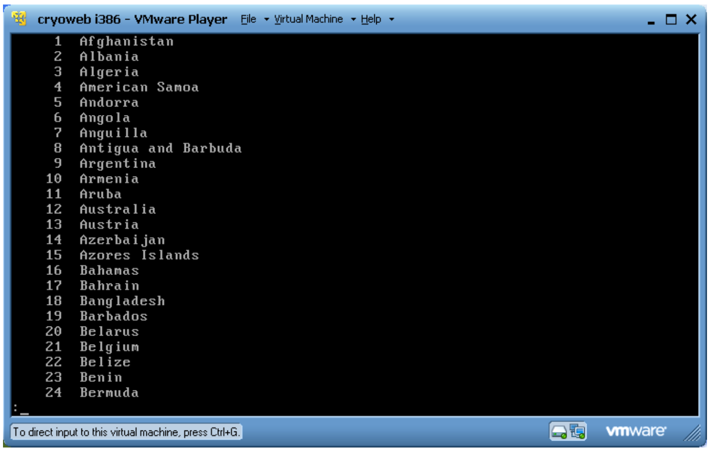
You will be guided to the sub-menu, shown in Figure 3.19. Choose the hour, you want to get the cron job executed and activate it. *Quit* brings you back to the main menu. The dump and restore options, especially the time driven daily dump, can help you to save the important data of your appliance, the database content. This does not replace a backup policy for your host or network.



```
[Q]uit
[D]isplay countries to select
[C]ountry selection

Task to perform: _
```

Figure 3.20: Select a country for CryoWEB installation

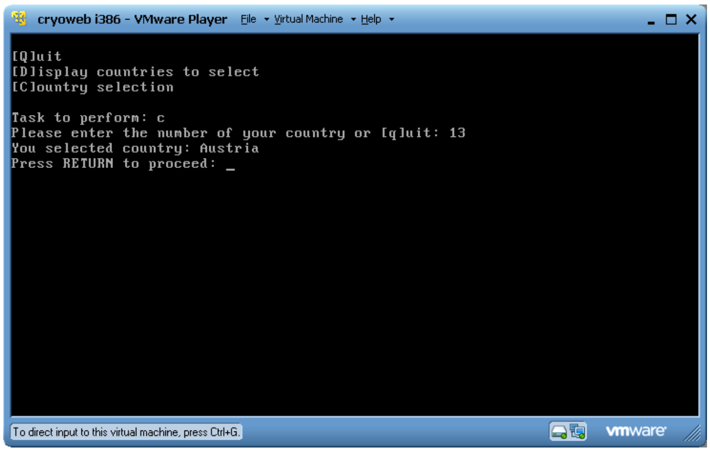
The *Select your country* option must be used right after the installation of the appliance to set the correct country for the software. This option leads you to a sub-menu (Figure 3.20). Use the *Display countries to select* option to find the number of your country in the list, e.g. 13 for Austria in Figure 3.21.



```
     1  Afghanistan
     2  Albania
     3  Algeria
     4  American Samoa
     5  Andorra
     6  Angola
     7  Anguilla
     8  Antigua and Barbuda
     9  Argentina
    10  Armenia
    11  Aruba
    12  Australia
    13  Austria
    14  Azerbaijan
    15  Azores Islands
    16  Bahamas
    17  Bahrain
    18  Bangladesh
    19  Barbados
    20  Belarus
    21  Belgium
    22  Belize
    23  Benin
    24  Bermuda
:_
```

Figure 3.21: List of countries with their numbers

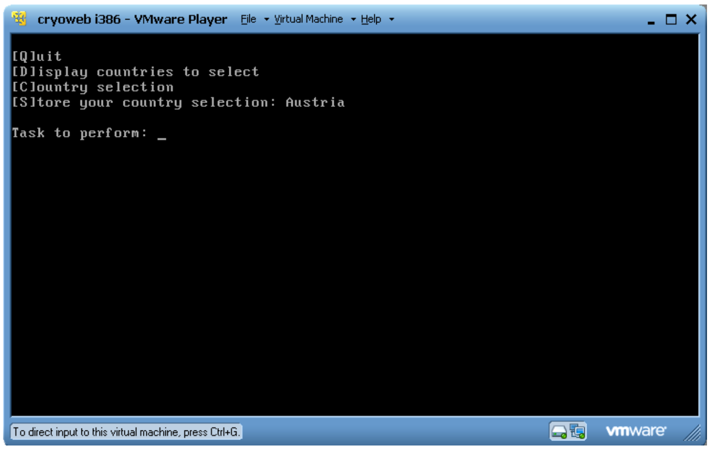
Then use this number in the *Countries selection* option as shown in Figure 3.22.



```
[Q]uit
[D]isplay countries to select
[C]ountry selection

Task to perform: c
Please enter the number of your country or [q]uit: 13
You selected country: Austria
Press RETURN to proceed: _
```

Figure 3.22: Country Austria selected for the software

Now, another item is added to the sub-menu (Figure 3.23). Choose this option to save the settings in the software.



```
[Q]uit
[D]isplay countries to select
[C]ountry selection
[S]tore your country selection: Austria

Task to perform: _
```

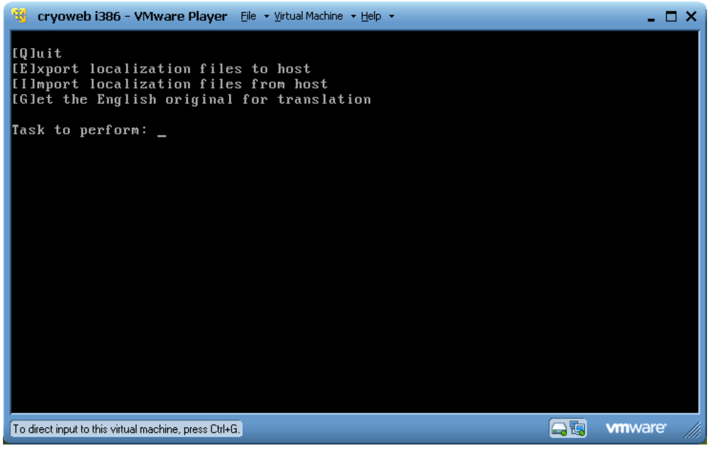
Figure 3.23: Store the country selection software

On the example shown in Figure 3.23 the database and software will be configured for use in country Austria. However, this will not translate the application's interface in the local language, e.g. German for Austria.

Note: You must choose a country before you start working with the CryoWEB page, but this can be done only once. Thus, if you set a wrong country for the installation, you must make a new installation, i.e. download the appliance file, run it in VMWare Player, or VirtualBox and select the country.

The *Net address display* option in the main menu displays again the information of the initial boot screen, shown in Figure 3.6.

The *Localization files* option is used for exporting and importing the localization files in CryoWEB (Figure 3.24). With the *Get the English original for translation* option the user can download the English source files, to be used as template for translation. The *Import localization files from host* option is used for uploading the translated files back into the appliance. The *Export localization files to host* option is used when the user wants to correct something in the translation. With this option the localization files for a certain language are downloaded in the shared folder on the host system. As such the **G** option is a shortcut for the **E** option with language en.



```
[Q]uit
[E]xport localization files to host
[I]mport localization files from host
[G]et the English original for translation

Task to perform: _
```

Figure 3.24: Export or import files for translation of the interface

For more details see Section 4.

For really rare cases, when it would be good to have direct access to the appliance, an administrative account is provided. The username is *cryo* with the initial password *ccc*. Please use this account only, if you really know what you are doing and have some experience with Linux systems!

4 Localization of CryoWEB

CryoWEB works by default in English, which probably will suit the needs of most international genebanks. However, there is also the option to translate the interface into another language, e.g. the local language of the country. This option will require additional effort and must be very carefully used as an incomplete translation might lead to inoperability of the CryoWEB software. The complexity of setting a new language in the appliance speaks for finding the support of a system administrator with knowledge of GNU/Linux OS.

The major part of the localization is done via localization files for each language. These are plain text files in UTF-8 encoding and should be edited with a UTF-8 capable text editor, e.g. EditPad on Windows, Kate or Kwrite on Linux. The files must not be edited with MS Word or other editors which may change the format or the encoding of the file. Moreover, you should ensure that the end-of-line (EOL) characters are kept in the GNU/Linux way - CR+LF. Alternatively, you might use an advanced text editor which handles the EOL characters transparently.

Each localization file has a specific structure. If the structure of the file is broken, the whole CryoWEB web page will not be operational. For example, omitting even a single character like inverted commas in the labels translation may corrupt the file structure. Thus, if you have any doubts, it is advisable to consult an experienced user.

If you want the CryoWEB page in a language other than English you need to provide the following 7 files in that local language on the appliance:

1. /home/cryo/dagenbank/etc/dagenbank_doc_bg.xml
2. /home/cryo/dagenbank/etc/dagenbank_doc_screen_bg.xml
3. /home/cryo/dagenbank/etc/dagenbank_doc_layout_bg.xml
4. /home/cryo/dagenbank/www/report/CryoLocalization_bg.properties
5. /home/cryo/dagenbank/www/jsript/cryo_l10n_bg.js
6. /home/cryo/dagenbank/lib/Apiis/I18N/L10N/bg.mo
7. /home/cryo/dagenbank/www/doc/about_bg.html

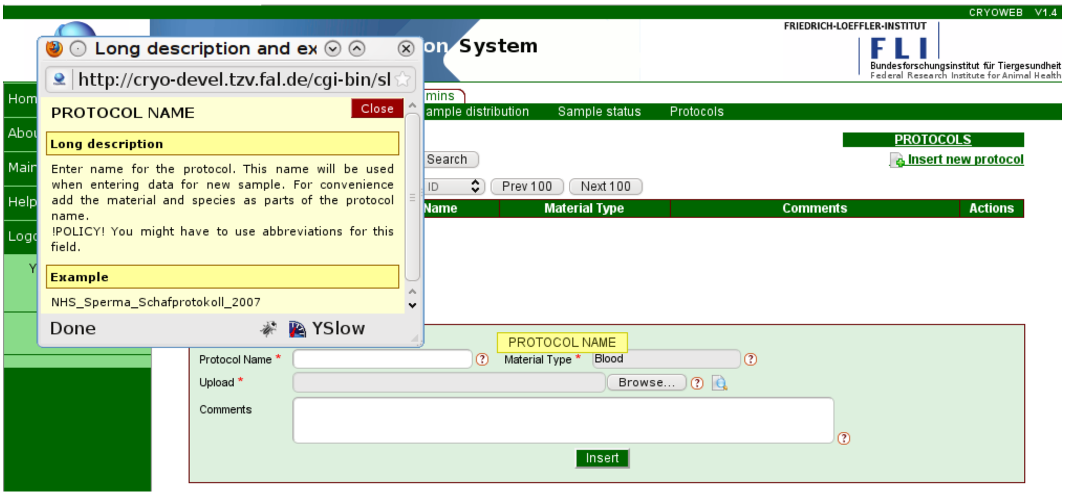
4.1 Copying the localization files to the translator's computer

There are two situations where you need to copy localization files from the appliance to the host machine. In the case of a fresh appliance you have to download the original files, which are in English and use them as a template for the translation. In case part of the translation was already done and there are localization files in your language uploaded to the appliance, you may directly download them and continue with the translation.

The English original files can be downloaded on the host machine by using the **vmadmin** account in CryoWEB appliance. After you log-in into the guest OS choose from the menu **L** for **Localization files**, then **G** for **Get the English original for translation**. If everything is OK the seven files dagenbank_doc_en.xml, dagenbank_doc_screen_en.xml, dagenbank_doc_layout_en.xml, CryoLocalization_en.properties, orig_en.mo, about_en.html and cryo_l10n_en.js will be copied into your shared folder where you can proceed with the translation.

If there is already a translation in your language, you can copy the respective files to the shared folder. Log in the appliance OS as user vmadmin, then choose from the menu **L** for **Localization files**, then **E** for **Export localization files to host**. If everything is OK the seven files dagenbank_doc_bg.xml, dagenbank_doc_screen_bg.xml, dagenbank_doc_layout_bg.xml, CryoLocalization_bg.properties.utf8, bg.mo, about_en.html and cryo_l10n_bg.js will be copied to your shared folder where you can continue with the translation (the example is for the Bulgarian language).

In both cases you can follow the copy process on the appliance screen, where also error messages will be printed.



Enter name for the protocol. This name will be used when entering data for new sample. For convenience add the material and species as parts of the protocol name.
!POLICY! You might have to use abbreviations for this field.

NHS_Sperma_Schafprotokoll_2007

Material Type * Blood

Figure 4.1: The tooltip and context help for the field Protocol Name

4.2 Translation of the fields context help

The context help (as shown in Figure 4.1) is kept in two files in XML format. These are: dagenbank_doc_<iso_lang>.xml and dagenbank_doc_screen_<iso_lang>.xml, where <iso_lang> is the standard language code. For example the files for English are named dagenbank_doc_en.xml and dagenbank_doc_screen_en.xml. If the interface is to be translated in Bulgarian, the respective files will be dagenbank_doc_bg.xml and dagenbank_doc_screen_bg.xml.

Both files have a uniform structure:

```
<?xml version="1.0" encoding="UTF-8" standalone="yes"?>1
<!DOCTYPE documentation SYSTEM "dependent_template.dtd">
<documentation>
   <general LANGUAGE="EN"></general>
   <table name="protocols" struct_type="optional">
      <column name="protocol_name">
        <long_description>Enter name for the protocol.
           This name will be used when entering data for new sample.
          For convenience add the material and species as parts of th
          protocol name. !POLICY! You might have to use abbreviations
          for this field.
        </long_description>
        <examples>NHS_Sperma_Schafprotokoll_2007</examples>
          <description>PROTOCOL NAME</description>
          <comments></comments>
          </column>
      ...
   </table>
 ...
</documentation>
```

In XML the elements of the document are identified by tags. A tag is the text between angled brackets, i.e. XML tags open with the < symbol and end with the > symbol. For example <documentation>, <general>, </general>,<table>, <column>, etc. are tags. The tags usually come in pairs - opening and closing tag, e.g. <column></column>.

In the context help files there is one table element for each database table. This element consists of one or more column elements. For each column element four elements are defined: long description, examples, description and comments. The text in the description element is shown as a tooltip when the user positions the mouse cursor over the help icon near the respective interface field. The text from the long description and examples elements are combined and shown in a pop-up window when the user clicks on the help icon near the respective interface field. The comments element is not shown on the screen and is used for remarks from/to the translator.

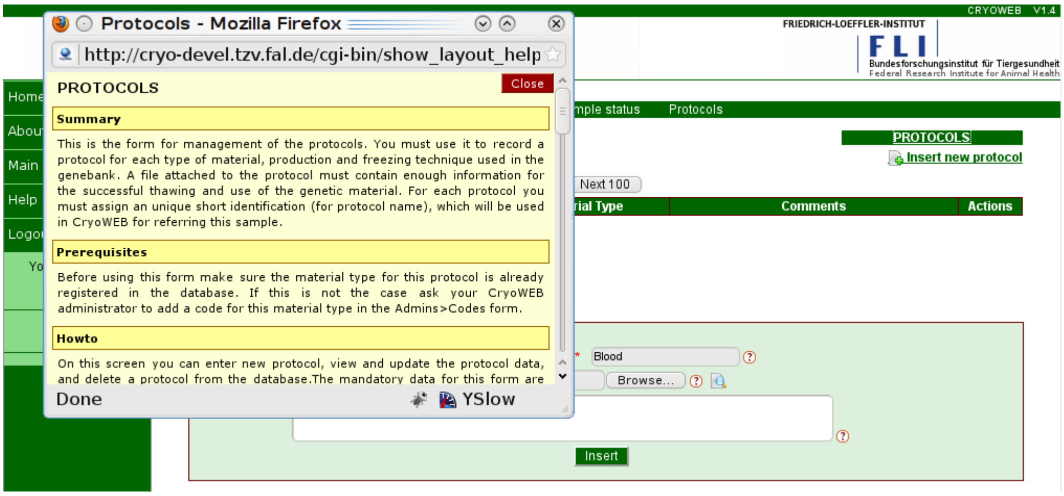
To translate the fields of the context help, copy the files dagenbank_doc_en.xml and dagenbank_doc_screen_en.xml to dagenbank_doc_bg.xml and dagenbank_doc_screen_bg.xml, respectively (the example is for Bulgarian language). In the '_bg' files overwrite the English text in the long description, examples, description elements with the local language version. If you edit the file with a text editor (these files can be also edited with a XML editor, but it should support Unicode

UTF-8 encoding), there are several special characters which should be referenced by entities. The entities for the most frequently used characters are given below. As an example, whenever the character '<' is to be shown it must be replaced by the 4 characters '<':

Character	XML entity
<	`<`
>	`>`
&	`&`
‘‘	`"`
’	`'`

4.3 Translation of the forms context help

The context help for each form (as shown in Figure 4.2) is kept in the dagenbank_doc_layout_<iso_lang>.xml, where <iso_lang> is the standard language code. For example the file for English is named dagenbank_doc_layout_en.xml. If the interface is to be translated in Bulgarian, the respective file will be dagenbank_doc_layout_bg.xml.



PROTOCOLS

Summary

This is the form for management of the protocols. You must use it to record a protocol for each type of material, production and freezing technique used in the genebank. A file attached to the protocol must contain enough information for the successful thawing and use of the genetic material. For each protocol you must assign an unique short identification (for protocol name), which will be used in CryoWEB for referring this sample.

Prerequisites

Before using this form make sure the material type for this protocol is already registered in the database. If this is not the case ask your CryoWEB administrator to add a code for this material type in the Admins>Codes form.

Howto

On this screen you can enter new protocol, view and update the protocol data, and delete a protocol from the database.The mandatory data for this form are

Figure 4.2: The context help for the protocols form

In the context help files there is one layout element for each screen sub-tab. This element consists of four elements: title, summary, prerequisites, howto. The text from these elements is combined and shown in a pop-up window when the user clicks on the label of the layout.

The forms context help file, which is also in XML format, is structured as follows:

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE documentation SYSTEM "help.dtd">
<documentation>     <general LANGUAGE="EN"/>
    <layout name="protocols">
      <title>Protocols</title>
      <summary>This is the form for management
                 of the protocols. ...
      </summary>
      <prerequisites>Before using this form
                     make sure the material type
                                       ...
     </prerequisites>
     <howto> On this screen you can
                               ...
              For detail explanation of a certain field click the
              <!-- Keep this text unchanged -->
             img_open ../images/icons/demoicon.gif img_close
               <!-- End of fixed text -->
           icon next to it.
     </howto>
    </layout>
    <layout name="animal">
        ....
    </layout>
</documentation>
```

To translate the context help copy the dagenbank_doc_layout_en.xml file to dagenbank_doc_layout_bg.xml (the example is for Bulgarian language). Then, overwrite in dagenbank_doc_layout_bg.xml the English text in the title, summary, prerequisites and howto elements with the local language version. If you edit the file with a text editor (these files can also be edited with a XML editor, but it should support Unicode UTF-8 encoding), entities have to be used for the special character (see 4.2). There is also text which must not be changed/translated. Such text is surrounded with the comments <!– Keep this text unchanged –> and <!– End of fixed text –>. You must not change this text and the surrounding comments.

4.4 Translation of the interface labels

The interface labels are stored in a <iso_lang>.mo localization files, e.g. de.mo for German language. The structure of these files is different from the context help files, in fact the .mo files are not XML files.

In this file the lines starting with # are comments and are ignored. Each interface string to be translated is represented in a line starting with msgid, e.g.

```
" or copy the URL in GoogleMaps: "
```

The translation into the local language must be written in the next msgstr line, e.g.

```
"oder die URL in GoogleMaps kopieren:"
```

If there is no translation, like for the message "GENEBANK STATISTICS", then the original English text is shown on the screen. The msgid strings must not be changed, as this is the link with the respective labels in the software code.

An excerpt from interface labels file is shown below:

```
#: lib/KMLReports.pm:107
msgid " or copy the URL in GoogleMaps: "
msgstr " oder die URL in GoogleMaps kopieren:"

#: lib/XMLConversion.pm:273
#. ($model_file)
msgid "Cannot open file %1"
msgstr "Kann die Datei %1 nicht öffnen"

#: lib/Labels.pm:610 lib/Labels.pm:616
msgid "GENEBANK STATISTICS"
msgstr ""
```

There are parameters in some of the English strings. These are marked with the % sign, e.g. "Cannot open file %1". During the execution of the code the software will replace parameter %1 with the respective value, e.g. "Cannot open file DS33.dat". When translating such strings the parameter placeholder must be preserved, however, its position in the translated string may differ due to the local language rules.

4.5 Translation of the report labels

The labels for the PDF reports are stored in properties files. These files are named CryoLocalization_<iso_lang>.properties, e.g. CryoLocalization_bg.properties for the Bulgarian language. However these files are not very convenient for direct manipulation by the user, therefore they are converted to UTF-8 encoded CryoLocalization_<iso_lang>.properties.utf8 file. In other words you have to open the CryoLocalization_en.properties file in an editor and save it as CryoLocalization_bg.properties.utf8 (for the Bulgarian language). Then translate this file and copy it to the shared folder on the host system. If you use the vmadmin menu to upload this file to the guest system, it will be automatically converted to Unicode-encoded CryoLocalization_bg.properties file.

The structure of the file is as follows:

```
# Locale  for samples_statistics.jrxml
r001.title=Animal Samples Report
r001.animal_code=Animal ID
r001.species=Species
```

The lines beginning with # are comments and are ignored by the software. The other lines contain key-value pairs. The key is on the left side of the equal sign, and the value is on the right. Each pair is on a separate line. The key should be kept intact and the value must be translated in the local language, e.g. r001.species=Spezies.

4.6 Translation of the Javascript messages

The localization file for the messages used in the Javascript are named cryo_l10n_<iso_lang>.js, e.g. cryo_l10n_de.js for German.

The structure of the file is shown below:

```
var cryo_l10n= {
   'messages': {
          1:'Are you sure that you want to execute this action?',
          2:' this data?',
          3:'Nothing to update or insert ',
          4:'Sorry, passwords do not match',
          5:'Are you sure you want to remove record from the database'
          6:'Generating report...',
          7:'Value already exists',
          8:'Error in Javascript !',
          9:'No such file in the database'
     },
          'Insert':'Insert',
          'Update':'Update',
          'Move':'Move',
          'Remove':'Remove',
          'Add':'Add',
          'View':'View'
};
var  vDelete='Delete';
var  vInsert='Insert';
var  vUpdate='Update';
var  vRemove='Remove';
var  vMove='Move';
var  vAdd='Add';
var  vView='View';
```

In this file there are three groups of strings to be translated. The first group contains the messages numbered 1 to 9, e.g. 2: 'Are you sure that you want to execute this action?'. Here the English version of the strings in quotes should be replaced by a translation in the local language. The second group is formed by the strings below the numbered messages, e.g. 'Move':'Move'. Here the translation will replace the string on the right side of the column, e.g. 'Move':'Verschieben'. The last group describes the variables defined in the bottom of the file, e.g. var vMove='Move'; . In the third group the translation should replace the English text on the right side of the equal sign, e.g. var vMove=Verschieben';. It is important that the translations of the third group match the respective translations of the interface labels.

4.7 Translation of the About text

You can also translate the About web page (Figure 2.3) of the CryoWEB software. This page is hardcoded in the file about_<iso_lang>.html, e.g. about_en.html for English. Copy the file about_en.html to about_<iso_lang>.html, where iso_lang is the ISO code of your language. Then translate the text, preserving the HTML tags intact.

4.8 Uploading the localization files to the CryoWEB guest OS

To upload the localization files to the appliance, copy all of them to the shared folder. Thus, if you have translated in Bulgarian language you must have the following seven files in the shared folder on the host OS: dagenbank_doc_bg.xml, dagenbank_doc_screen_bg.xml, dagenbank_doc_layout_bg.xml, CryoLocalization_bg.properties.utf8, cryo_l10n_bg.js, about_bg.html and bg.mo. Then go to the appliance and login as user vmadmin. From the menu choose **L** for **Localization files**, then **I** for Import localization files from host. The files will be uploaded in the appliance copied to the right locations. The CryoLocalization_bg.properties.utf8 will be converted to CryoLocalization_bg.properties. Keep in mind that the uploaded files will overwrite the existing files in the appliance .

4.9 Translation of the drop-down list items

To translate the elements of the drop-down lists, e.g. the allowed status values, or the sex codes you have to be signed in as CryoWEB manager. Open the codes form via **Main menu** ▷ **Admins** ▷ **Codes**. Choose from the **Class** name list the group of codes (one class represents one drop-down list type) and click on the **Search** button. For each record in the results table click the **Update** action icon, then replace the values for the **Short name** and **Long name** with the translations in the local language and click the **Update** button to submit the form. When finished with one class, continue with the next until all required classes (AVAILABILITY, BREED, COUNTRY, CRYO_TYPE, LANGUAGE, SEX, SPECIES and VESSEL_TYPE) are translated.

4.10 Additional requirements to enable a new language

After all files have been translated and uploaded into the appliance you need to register the new language in the software. This requires additional settings in one of the configuration files in the guest OS. To make these settings, log in as user cryo in the appliance. Then open the file L10N.pm for editing, e.g. with vi editor:

```
vi /home/cryo/apiis/lib/Apiis/I18N/L10N.pm
```

and add the line (replace bg with your language)

```
bg         => [ 'Gettext' => 'Apiis/I18N/L10N/bg.mo', 'Auto' ],
```

in the beginning of the file, just below the similar line for en and de languages:

```
use Locale::Maketext::Lexicon {
        en => [ 'Gettext' => 'Apiis/I18N/L10N/en.mo', 'Auto' ],
        de => [ 'Gettext' => 'Apiis/I18N/L10N/de.mo', 'Auto' ],
        bg => [ 'Gettext' => 'Apiis/I18N/L10N/bg.mo', 'Auto' ]
```

5 Maintenance of the CryoWEB installation

Being a live system, CryoWEB needs to be maintained just like any other live information system. The main blocks needing attention are:

- backup
  - the complete appliance: backup and restore
  - database content: database dump
- software updates
- reporting bugs

5.1 Backup

Just like any other system also CryoWEB requires a backup strategy. Here the same principles apply: the user needs to be guarded against total loss of the storage media, i.e. a disk crash or theft, and secondly should be able to revert to a previous version of the database content in case of actually unintended modifications or deletions. Therefore, CryoWEB should be included in the standard backup strategy of the institution where it runs.

Because CryoWEB is installed as a virtual appliance, it requires a few special considerations. The appliance presents itself towards the host operating system as a normal – however very large – file. If the host system has a backup strategy in place, the appliance will be automatically part of it. Whenever the appliance is started, it will write some logging information, thereby modifying the appliance file which in turn will lead to this file being backed up, although no actual data in the database has been modified. Therefore, it may make sense to exclude the appliance file from the daily host system backups, but to make a manual backup after the appliance was configured or reconfigured.

A different strategy has to be applied for the backup of the data content stored in the CryoWEB database. Here, the user should make a provision to move the database content out of the appliance into the file system of the host system. Once it is there, the regular backup strategy of the host system would take care of backup. Two options exist here, manual, and automated dumping of the database from the guest to the host system. In both cases the user has to log in the CryoWEB guest operating system with the **vmadmin** account. For immediate dumping, the user should use the [D] option: *Dump the database*, which will create a database dump (named **cryoweb_export.dump**) in the shared folder of the host system. The other option is to schedule the dumping to be executed automatically once per day. This is done by selecting *Cron: run dump regularly once a day* and following the submenu. For more details see section 3.5. Please note, that the next dumping simply overwrites the file **cryoweb_export.dump** in the host OS, thus if the user wants to keep the old database dumps, she should rename the file **cryoweb_export.dump**. For reloading a dump file, the user should copy it into the shared folder under the name **cryoweb_import.dump**. Then she should log in as vmadmin user in the CryoWEB operating system and execute the *Restore the database* command.

5.2 Software updates

Updates in software may be required in the future, e.g. in case of bug fixes and adding new features. The approach for software updates we took with CryoWEB is based on producing each time a new appliance which includes the last changes. If a user wants to use this new appliance, she has to export the database from her old appliance in a dump file, then replace the old appliance with a new one, and then import the data in the new appliance.

Upgrading to a new appliance, when the interface was translated in a local language, is more complicated. In such a case you have to export from the old appliance also the localization files and export from the new appliance the English templates. Then, you must compare file by file the old translations with the new templates, merge any missing strings from the English templates into localization files and translate these strings. When the localization files are ready you must upload them in the new appliance (see section 4.8) and make the additional settings to enable the local language in the new appliance as described in section 4.10.

5.3 Reporting bugs

Even the most elaborated software may contain some bugs. The code of CryoWEB is pretty mature and has been in use since years, but it will, most likely, still have bugs. Bug reports for CryoWEB can be submitted by sending email to cryoweb-bugs@tzv.fal.de, where they will be processed by the respective developer. Please note that this e-mail is only for bug reports, if you need assistance or support contact the maintainer of your database.

In reporting a bug, be precise, clear and do not report more than one bug in a single mail. It is very important to separate clearly the facts from the speculation. A bug report should contain as a minimum description of three basic elements - what you did, what you expected to have happened and what actually happened. If you noticed a bug when using the web page, report also what browser you have used, which virtualization software are you using (VirtualBox, VMWare Player) along with its version, the host operating system.

5.4 Loading historic data

In many cases, new users of CryoWEB will have data on their cryo material available in electronic formats. Then the question arises, how to get that information into CryoWEB. In principle, there are two paths for migration to CryoWEB: entering all previous data manually or loading this data through a program. In case you have already a large amount of genebank documentation in electronic form, loading this data via software is a better solution. The main steps involved in such loading are:

1. Loading of the species/breeds data.
2. Loading of the protocols.
3. Loading of the donor animals.
4. Loading of the storage hierarchy.
5. Loading of the samples data.
6. Loading of the samples distribution data.

However, this is an interactive process, which includes manual cleaning of errors at each step. This depends also heavily on the initial settings and policies you choose for your genebank documentation rules. In case of large data volumes you might want to contact the authors of CryoWEB for advice, or ask the user community in our forum (see section 5.5).

5.5 Requesting help and exchanging experience

The CryoWEB software has already been installed in several countries and a number of national and international training workshops took place. Thus, there is already a group of experienced users who can give advice in regards of the genebanks management and documentation. To have a uniform communication platform for these users and also for contact with the group of developers and maintainers of CryoWEB software a mailing list was set up. The list can be accessed at http://mailman.tzv.fal.de/mailman/listinfo/cryoweb. The list is open for reading to the general public and the list archives can be directly accessed via http://mailman.tzv.fal.de/pipermail/cryoweb/. However, if you want to post a message on this list, you must be a list subscriber. The registration process is very simple and requires only email address and password. You can subscribe on the list web page: http://mailman.tzv.fal.de/mailman/listinfo/cryoweb in the section **Subscribing to Cryoweb**. We require the users to register before posting to reduce the amount of SPAM messages on the list. You can unsubscribe anytime by using the **Unsubscribe or edit options** button in the lower part of the list page.

6 Minimal data set and policies required by CryoWEB

6.1 Minimal data set

CryoWEB has been developed with the objective, to provide an out of the box genebank recording and management system that should work for all species and material types anywhere in the world. Accordingly, a minimal dataset has been developed which meets these requirements. As the database structure is intended to be used as is, no species nor material type specific data should be collected, but only data elements that are – at least in principle – available for all material types and species. There are three major blocks of information: the first for the donors, the second on the sample and thirdly unspecific data.

Donor: Here we deal with animal specific information of any species. Often available for any animal are the species, the animal ID plus its parents, a birth date, sex, and breed or genetic group, plus an organization or person with possibly more information on this particular animal like a breed society or a collector of the material. Thus, these data elements are modelled in the database structure as fields which at least in principle can be collected for any species anywhere in the world.

Often phenotypic data are considered important. But recording these in a decomposed database structure cannot really be organized in a meaningful manner independently of species and locations. Recording milk yield may be useful in a number of species, but certainly not for fowl. Likewise, description of the phenotype in terms of shape, color etc. are highly species specific. However, a scaled digital image can be viewed as an abstraction applicable and at least potentially available on each living animal. A digital color photo can easily be taken from an animal. If a large ruler is held up close to the animal while the photo is taken, ex post a substantial number of measurements can be derived from them, each specific for a given species, but all based on that same database field, i.e. the scaled digital image.

Adaptation to a certain environment is often considered an important property of breeds. While environments are difficult to describe in a general way applicable to all species and locations, world wide GPS coordinates – which can be obtained for each animal in principle – provide an elegant means of deriving this information later on: for a given set of GPS coordinates a location is precisely defined world wide. Given the appropriate maps, a large number of parameters can be obtained. Examples are: altitude, temperatures, rainfall, soil types etc. Thus, GPS coordinates have been added to the data structure specifying animals.

Depending on how developed a breed recording system is, a large amount of specific data will be available for donors. These may be pedigrees of varying depths, breeding values on certain traits, veterinary certificates, to name but a few. Clearly, the structure of this sort of information will not only be different among species, but even among breed organizations within species. As a result, for a generally applicable database system, the data elements cannot be decomposed into traditional searchable database fields. However, the provision of allowing to store a document as a binary large object (BLOB) much like an image also provides a way out here. If a user decides to store the animal's pedigree document and performance record card in the database, an archive can be created from the two original documents resulting in one data file which can then be loaded into the database. In this way, any electronic information can be "attached" to a donor, using the database as a kind of filing cabinet.

Often storing directly readable information (without having to go through a download of a BLOB, extracting the original file from the archive and then starting the appropriate helper program to read it) with a donor of unspecific kind seems desirable. This can most easily be achieved through the provision of text blocks in the database, that users can fill with any sort of textual information. Thus, **Comment** blocks are part of the database structure.

Samples will represent many different material types like semen, embryos, oocytes, somatic cells. Their treatment for later use will be very different and not at all uniform across the material. Thus, recording the minimum motility of semen and the treatment of blood samples prior to freezing in database fields will create a very complex database structure, which would have to be expanded (i.e. require programming) should a new material be added to the genebank. Much like is the case with the animals, BLOBs also provide a way out: For each sample, documents can be stored, as has been described for the donors. As before: we have again created an abstraction that works for each sample of any material type anywhere in the world, including material types not yet defined, where the detailed information needs to be written in that document by the user. As mentioned above, also here the comment text block provides for space for any sort of written text and notes.

Genebanks of animal genetic resources are a long term storage of genetic material of any kind. The conserved material is intended to be used in the future for the recreation of a breed, supportive breeding, or scientific purposes. This is only possible if the documentation system contains enough data to meet these purposes. The major requirements can be summarized in the following questions:

- Where is sample X?
- What samples are available from breed X?
- Who was the donor of sample X?
- Under what circumstances can sample X be used?
- What procedure should be followed to thaw and use sample X?
- What material is stored in location X?
- Where can material from animal X be found?
- How much material is left from donor X?
- What are the characteristics of the material in sample X?
- What are the characteristics of the donor of sample X?

The data required to answer the first 8 questions is crucial for the management and operation of the genebank. Accordingly, answers to these eight questions are considered the minimal mandatory data set in CryoWEB. A sample can only be documented in CryoWEB, if all the required data is available at the time of the data entry. The minimal set is uniform across species and material types and will be described in more details further in this chapter.

In regards to the last two questions in the list, the data needed for their answers is very specific to the material type and donor species. For example the phenotypic traits measured on a pig donor will be different from those measured on a horse, while usually different sets of characteristics are recorded for different material types. Furthermore, as the intended use of the material is far in the future, we also do not know what prospective users may be interested in. All of this has lead us to create a data structure of to be recorded traits, that is uniform across species and material types, thereby considerably simplifying the task of data recording and data entry [4].

Therefore, such data is not mandatory in CryoWEB and the user can enter it in the database using free text fields and archive files containing all the information considered relevant for the respective donor or sample as described above.

With this setup CryoWEB enforces documentation discipline on the managers of the genebanks, restricting as much as possible the cases of incomplete data. The minimal mandatory data set approach prevents many cases of unusable or lost material due to missing information and can be used as a model in the organization of the data collection scheme.

The minimal data set for a sample to be recorded in CryoWEB consists of:

1. Identification of the sample
2. Identification of the donor
3. Date of production
4. Type of material
5. Protocol for sample production and thawing
6. Type of vessel
7. Distribution of the sample units in the storage facilities

In the following, each of these 7 blocks will be described in more detail.

1. The *identification of the sample* has to be unique within the whole database and has to reflect the label on the vessel in which the sample is packed. For more details see the policy section below in this chapter.
2. The *identification of the donor* must also be unique within the database. The donor has to be registered as an animal in the database prior to the entry of sample data. To register a animal in CryoWEB the following data is required:
    - Animal identification
    - Species
    - Breed
    - Sex
    - Reference organization (which can supply detailed information for this animal)
3. The *date of production* of the sample is the date when the material was taken from the donor. It may differ from the date when the material was frozen (which is also recorded in CryoWEB, but as non-mandatory data).
4. A genebank will contain different *type of material* like semen, embryos, somatic cells, blood and possibly DNA.
5. For each sample, a file with detailed description of the methodology applied in producing and freezing the sample and the steps to be followed when thawing must be available. This is the *protocol* file which also has to be loaded in the database. However, if more than one sample is produced following the same procedures only one protocol is required for all of them. Typically, freezing and thawing protocols do not change often, but, instead, are valid for a number of years.
6. The *type of vessel* is the type of the packaging used for the sample. The presumption in CryoWEB is, that all sample units are packaged in the same type of vessel, e.g. only straws with same volume in case of semen.

7. One sample is usually divided into several parts, which are stored in different locations in the *storage* facilities. The distribution of the sample in the storage is recorded with the following items:

    - Location
    - Number of units in this location
    - Status of the units
    - Entry date

    The location is described as hierarchy of five levels, e.g. the storage place, tank, canister, compartment, cell. The purpose of the levels in the hierarchy is to pinpoint the position of the sample in the storage without additional external knowledge. Therefore, the levels must be chosen in correspondence with the organization of the storage facilities. This question is also discussed in the policy section below.

    Usually a sample (like a bunch of straws) in a national genebank is divided into several parts, depending on their legal status. Part of the units is defined as long-term 'core' reserve, another part is a pool for supportive breeding in the near future, and, sometimes, a third part is intended for scientific purposes or for free use. For each group of sample units in one location, the user has to enter their legal status.

6.2 Policies

CryoWEB provides the general framework for documentation using its inbuilt business rules to reduce the errors during data entry. However, it is the user, who is responsible for the correct data entry. For example, the software can check, if the sample identification is missing, or duplicate, but cannot prove if the entered identification reflects the reality. There are several places in CryoWEB where the user has to take a decision about the data to be entered, e.g. the animal identification, samples identification, storage facilities. A good example is the identification of the animal, as there are often more than one ID for the same animal during its life. In CryoWEB, the animal is registered with one ID and therefore the user has to choose which of the multiple identifications to use. Especially in gene banks which have repositories of frozen material prior to setting an information system, this is can be an issue as in the various documents different animal IDs may be used. Moreover, the genebank is usually a collective effort of several organizations and persons, and each of the participants must know what ID to use when searching for an animal. Therefore, a clear system of rules (policies) is needed in the process of preparing the data for entry in CryoWEB. This system of policies must be familiar to all users of the genebank, and everybody should follow it. Failing to follow the rules will not prevent the user from entering data in the database, but will create inconsistencies, which may lead in the future to problems in finding the data.

6.2.1 Animal ID

Historically, farm animals have often been identified with multiple identifications like the notch number, herdbook number, etc. These numbers were also reused after the animal's death. Thus, the same identification was used for different animals in different time periods. In recent years, a process of consolidation has started giving each animal a unique lifelong ID, e.g. the 12 digit EU cattle ID. Nevertheless, collections containing old material will have also the problem of animal identification also in cattle.

CryoWEB has inbuilt requirement for a unique Animal ID within the whole database, i.e. across species and breeds. This requirement can be met with assigning an automatically generated number for each animal donor and this number to be linked to a real-life identification. However, the users still prefer to use directly a real ID for the animals. In such case a system of policies is needed to address the following issues:

- Which animal ID to be used in CryoWEB? As the animal may have several identifications, the user must know which one to use for data entry and searching. A solution here can be the definition of ordered list of identification types for each species, e.g. herdbook number, farm number, name, etc. Then, the first available identification in that order will be used in the database.
- Even if the decision has been taken to use the herdbook number, its composition is not necessarily clear. Often a herdbook number in sheep or in pigs is a four digit number. The breed society usually ensures that no other live animal exists with this ID. This implies, that there may very well be an historic animal with this code. Furthermore, uniqueness may be only within breed, while other herdbook societies also use the – rather limited – 4 digit number space. Therefore, to ensure uniqueness with CryoWEB the ID may need to contain elements like: herdbook society, species, breed, sex, year. Defining the exact order requires a genebank policy. But not only the order is important: if uniqueness can only be ensured by stringing together pieces of information, it has to be decided how they are linked. On animal certificates often the herdbook society, species, breed, sex, year, and herdbook number is printed in one line, separating the elements by blanks for readability. When the animal ID gets entered in CryoWEB, one string needs to be provided. The elements may get connected through '-' or '_' or a blank. Whatever it is, it should be the same rules in the complete database. Only then it will be possible to locate a sample in the database, if someone from a certain breed society asks for information on a Texel ram with the ID 1234 from 1996.
- How to deal with duplicated identifications? If the user tries to enter a new animal (e.g. with ID Herodes), which is already occupied by another animal recorded before in CryoWEB, the system will refuse to register it with the error message "Duplicate key violation...". In such case the ID of the new animal has to be changed to become unique. This can be done in many ways,

e.g. appending a letter at the end - Herodes_a, or appending the birth year - Herodes_1980, or even a combination of the birth year and a letter, in case there are several animals born in the same year and having the same ID - Herodes_1980_a. We would suggest to append additional information at the end of the identification (and preserve the real ID at the beginning) as one of the CryoWEB features allows the user to search animal ID by the first characters. Moreover, the animal IDs are used in the web interface as elements of a drop-down list, and keeping the real ID at the beginning of the sting makes the animal easier to be found in the list. Again, the appropriate policy for the particular setup must be chosen and documented by the genebank administrator.

6.2.2 Organization

The CryoWEB system contains also a contact folder for organizations and persons involved in the genebank. It collects as mandatory data the contact details of the organizations holding detailed information about the donors. Such organizations (or persons) can be used as a starting point in acquiring additional details for the donor, or requesting more material. As the organization names are usually long, a short meaningful identifier is used instead in the drop-down lists on the CryoWEB interface. This identifier must be unique within the CryoWEB system. A special policy is required to define how this identifier is created by the user. A possible option for a organization identifier is the abbreviation of the name, e.g. FLI for Friedrich-Loeffler-Institut. In case of a person name it is not so straight forward to create such an identifier. For example, if there are two farmers called John Smith the two identifiers have to be different. This can be achieved by appending numbers, e.g. JSmith1 and JSmith2, but this does not help the user in resolving ID to name. A more meaningful option may be appending the town, the position, or other information helping to resolve the ID. But, again, it is important, that the rule is generally known and followed during data entry and search.

6.2.3 Sample ID

The sample ID is one of the most important pieces of information in the database as it provides the link to all data recorded for a certain sample. In CryoWEB, sample ID must be unique across material types. The sample ID must also reflect the label on the vessel in which the sample units are packaged. Usually this label is used as ID, but similar to the animal ID, policies are needed to deal with the following issues:

How to enter a sample ID in the database? In case of semen the label on the straw follows nowadays a standard and often looks like `MA 015 KR S Snh S03 Mariensee T-000141 Le 24.11.03`. It is not advisable to use this string as it is as sample ID (i.e. no rules) with the blanks included. Why is this so? If a user wants to locate information on a specified sample in the database, the exact string used during data entry also needs to be used for retrieval. Thus, if entered with blanks included, the sample will not be found if the sample ID is used without the blanks. A possible way to prevent such errors is to have a rule describing on which position the user must put spaces and the exact number of spaces. Alternatively, the rule may require the replacement of all spaces with underscore, e.g. `MA_015_KR_S_Snh_S03_Mariensee_T-000141_Le_24.11.03`. Further, if the label is split on two lines the rule should be to join them into a single string.

How to deal with duplicated identifications? Especially in old collections the vessels are sometimes labeled with the consecutive numbers which are unique only within the location and material type. Especially when samples from many collections are merged, as may be the case, when setting up a national genebank, the problem of duplicate vessel labels may occur. In such cases there should be a clear rule how to create from the vessel labels unique sample IDs. This can be done, e.g. by appending the date of production, and/or the material type, however the rule will be specific to the setup of the particular genebank where CryoWEB is used for documentation.

6.2.4 Geographic location of the donor

In CryoWEB the location of the donor animal in terms of GPS coordinates may be recorded as part of the non-mandatory data. This information can be used to present the geographical distribution of the donors from a single breed, thus, giving a nice visual impression of its geographical spread. However, this information is usually not available for the material which is already stored. In such case the location can be obtained indirectly via the address of the owner. Here, the manager has to set up a policy about the procedure to be followed in obtaining the coordinates of the donors locations.

Furthermore, the GPS coordinate system needs to be specified. The WGS84 is widely used and would be the standard of choice. Here, the user needs to ensure, that an address is resolved to this standard by choosing the corresponding system on the GPS gadget or the mapping system.

6.2.5 Data archive files

CryoWEB allows for each animal one archive of documents to be stored in the database. The content of such an archive file can be anything. The user can put there whatever she considers important for the donor, from birth certificate and veterinary exams, to station test and genetic evaluation results, e.g. BLUPs. It is important to use a standard format for the archive file, such that the file can be read also in the distant future. Examples are zip or the Unix tar. The content and format of the archive file for the particular setup should be described by the genebank manager. Details about each individual archive stored should be given in the record's text block.

6.2.6 Storage facilities

The storage facilities in CryoWEB are described as a hierarchy of five levels. The precise location of a sample in the storage facilities is then defined as a sequence of five elements - one element for each level. This general setup should be able to cover the most common types of cryocontainers and allow unique identification of a sample position. Depending on the specific setup of the genebank these five abstract levels must be mapped to a real storage facilities. How this should be done, is a matter of policy. The example below covers a typical situation for storing semen, which could be used as a general policy.

The first level of the hierarchy is usually the institution where the material is kept, e.g. ING Mariensee for the Institute of Farm Animal Genetics. The second level can be mapped to the cryo tank. Tanks are often numbered by roman numerals (I, II, III, IV etc.), but other identifications are also in use. The third level can be mapped to the canister within the tank. In the case of ING the canisters are identified with Arabic numbers. Each canister has several levels. The fourth abstract level can be mapped to the level inside a canister. In such case the fifth and last level can be the goblet which contains the straws of the sample. Goblets are usually distinguished by color. In such setup the location of a sample in the blue goblet on level 2 of canister 8 in tank I in ING is described as ING>I>8>2>blue.

In case the storage facilities are organized in a different manner the levels have to be mapped accordingly. The important rule is that the last level should be chosen such that the user can quickly find the sample in it by sequentially searching its content for the desired sample ID.

In some cases the number of physical levels can be lower than five. In such a case one or more of the abstract levels have to be fixed and get a default value. Which levels to be fixed has to be decided by the genebank manager, generally it is advisable to fix the lowest abstract levels.

In other cases the physical levels are as the ones described in the example, but the goblets are all the same color, i.e. one cannot distinguish them. In this case the fifth level has to be fixed with a default value, e.g. '-'. The location of the sample will look like ING>I>8>2>-.

6.2.7 Units

In CryoWEB, a sample is defined as a one type material taken from a single donor on one day. The sample consists of multiple identical replicates or volume units. In case of semen these replicates are single straws, as the straws are equivalent to each other. In case of blood the sample is measured in ml. The abstract sample 'Units' recorded in CryoWEB cover the number of replicates or the amount of material. For different materials units may be different, but within materials, units must be the same. Thus, the blood samples should be always measured in the same units, irrespective of the breed or species. The units have to be defined for each material type by the genebank management and all users should enter data according to that definition.

6.2.8 Protocols

The main purpose of the stored material is to be used in the future. For each sample there should be enough information in the database, that will allow appropriate gentle thawing and use. To provided this information which may be needed after 20-30 years, CryoWEB attaches each sample to a 'protocol', describing the procedures followed in freezing the sample and the steps to be taken for thawing. The information is stored as an archive of documents or a single file, which may contain also data about the hygienic status at the time of collection (which probably will be outdated anyway in the distant future) and any additional data which seems appropriate for this type of material and conservation procedure. This document needs to be written by the genebank manager or by someone familiar with the material type under consideration. Again, a policy is needed what data has to be recorded in the archive and what name to be used for this protocol. The protocol name should be a short meaningful identification, which can be easily understood by the user. One possible way to generate such a name is to concatenate the material type, the species and the year of the protocol, e.g. NHS_Schafprotokoll_2003. This is an example from our institute, where NHS means 'Nebenhodenschwanzsperma' in German which was obtained from testis of rams post mortem (i.e. epididymal semen) in the year 2003. 'Schafprotokoll (= sheep protocol)' indicates a species specific freezing protocol.

A protocol is typically a text document which may or may not contain graphs or images. Thus, it may get written using some text processing software. Because of the long time horizon of a genebank, this document needs to be readable also after decades. This means, that the user needs to ensure that a program is available to read this document. Here, proprietary data formats are not a good choice. Imagine that a protocol text was written 15 years ago, then you may not be able to read this file now, as neither the operating system not the program is available anymore. As a general rule, only open formats should be used which can typically be handled by different programs, precluding use of software like MS-Word. Options would be the Open Document Standard (ODS) which is used by software like OpenOffice. Alternatively, ASCII texts can be used which are inputs to the typesetting system LaTex. Yet another option would be to store the document in PDF format, which in all likelihood will be readable also in the distant future. However, this may have the disadvantage, that the file cannot be modified easily, which may be a useful feature, if the current protocol is used as a basis for a modified one. Finally, an archive could be loaded as a protocol, comprising a PDF and a text processing document.

6.2.9 Legal status of the sample

Usually each sample is split in several parts, e.g. for long term conservation, for short term conservation, for scientific purposes, or for free use. The status of each part of the sample defines how and when material from that part may be used. There are three predefined status values in CryoWEB which should be mapped to the real setup of the genebank. The most important from them is the 'core' value. Material marked with that value is considered in CryoWEB a long term reserve, and the software will not allow the user to directly remove this material from the database. Moreover, for protection reasons, CryoWEB allows only storage of sample units with the same status in the lowest level of hierarchy. Thus, the long term and free straws of a semen sample must be stored in separate goblets. Keeping in mind these restrictions, the manager of the genebank must define a policy for the the meaning of the non-core status classes.

6.2.10 List of decisions to be taken

In this paragraph a summary of the decisions are listed that have to be taken by the genebank management. All documents should be sufficiently detailed and self contained, that any person can follow them.

1. Q: What breeds and species to register in the database?

   A: List of species and breeds .... Document_1
2. Q: What organization possibly supplying more information for a donor should be recorded?

   A: the answer may be different among the species or sources of material (herdbook/non herdbook/source without animal identification) ...... Document_2
3. Q: Which animal identification to be used in CryoWEB for a donor, their elements, their order and connecting character?

   A: for each ID system one set of rules; e.g. cattle, sheep, pigs .. Document_3
4. Q: How to deal with animals which have same identifications in real life?

   A: describe strategy that can/must be applied to each new identification to be entered if this one is already in the database.................... Document_4
5. Q: What ID to be used if the donor of a sample is unknown?

   A: a description of the action to be taken in this case.......... Document_5
6. Q: What to do if the species, the breed, or the sex of a donor are not known?

   A: define your policy .... Document_6
7. Q: Do you want to record the donor location and if yes, what coordinate system to use and what to do if the location is not known for a certain animal?

   A: give an exhaustive description, how to proceed .... Document_7
8. Q: Will you record an image from a donor and how this photo should be taken to allow measuring phenotypic traits from it?

   A: describe how to take the photo (aperture, distance to the object etc) and the scale, preferable with an example........................... Document_8

9. Q: What additional data to collect for the donors in the form of an archive file?

   A: scanned documents can be stored in this archive, state your policy probably for each species . . . . Document_9

10. Q: What should a protocol file for sample production contain and how should it be named?

    A: one document is required for each sample type, a typical genebank with cattle, sheep, pigs would require

    a) pigs – semen . . . . Document_10.1
    b) sheep – semen . . . . Document_10.2
    c) cattle – semen . . . . Document_10.3
    d) cattle – embryos . . . . Document_10.4
    e) all – somatic cells . . . . Document_10.5

11. Q: What are the definitions of 'units' for liquid material types like blood?

    A: ml for blood; requires one specification for each non-count material type! Document_11.1

12. Q: What identification to use for a sample?

    A: A complete description is required for each sample type! . . . . Document_12

13. Q: How to deal with samples having the same labels on their vessels?

    A: describe policy along the lines of duplicate animals . . . . Document_13

14. Q: How to describe the storage facilities as hierarchy of maximum five levels?

    A: specify all your storage tanks, internal setup . . . . Document_14

15. Q: What production and storage date to record in the database if either or both is unknown?

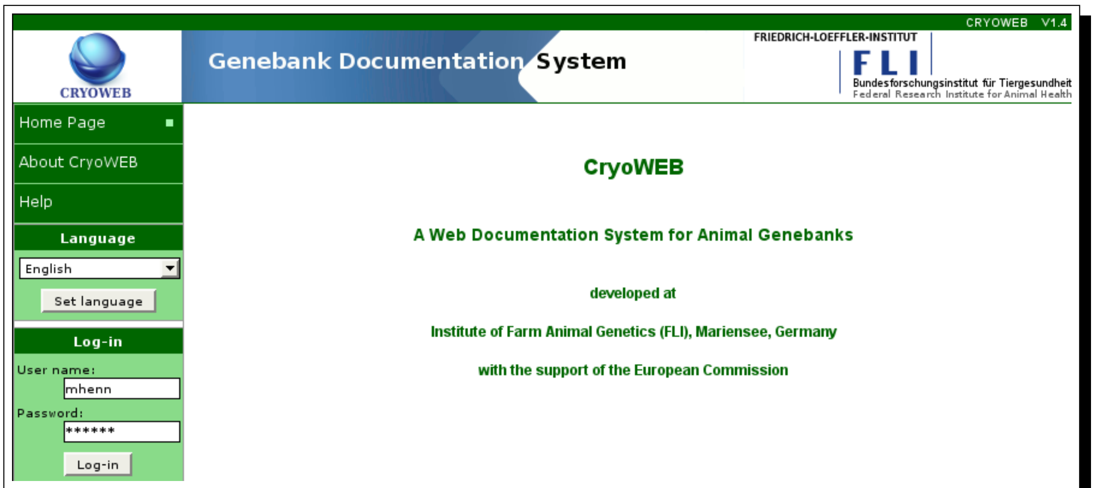
    A: may be needed for old samples . . . . Document_15

It is our view, that each genebank using CryoWEB must have an internal set of policies put down in these 15 different documents. Some of them will be rather short while others may have to contain a substantial number of pages as would be required for the protocols for each the sample or material type. Thus, the above list can be used as an outline which makes checking for completeness of genebank policy specification rather easy.

7 User's tasks

7.1 Logging in to the system

Access to the database is possible via any standard recent browser, Firefox being the most recommended one. To begin work with CryoWEB type the URL of your system in the Location Bar of the browser, and open the page. On the left side of the screen a language choice is offered. Choose the interface language from the drop-down list and click the **Set language** button, then proceed to the **Log in** section. To work with CryoWEB you must be logged in. Enter your user name and password (Figure 7.1) (provided to you by the administrator) and click the **Log-in** button to enter the CryoWEB home page.



Language: English

User name: mhenn

Password: ******

CryoWEB

A Web Documentation System for Animal Genebanks

developed at

Institute of Farm Animal Genetics (FLI), Mariensee, Germany

with the support of the European Commission

Figure 7.1: Log into the system

If the log-in was successful, you will see on the left side the menu items and below them, the login status. In case the login process fails, you will receive error message:

```
Authentication failed
```

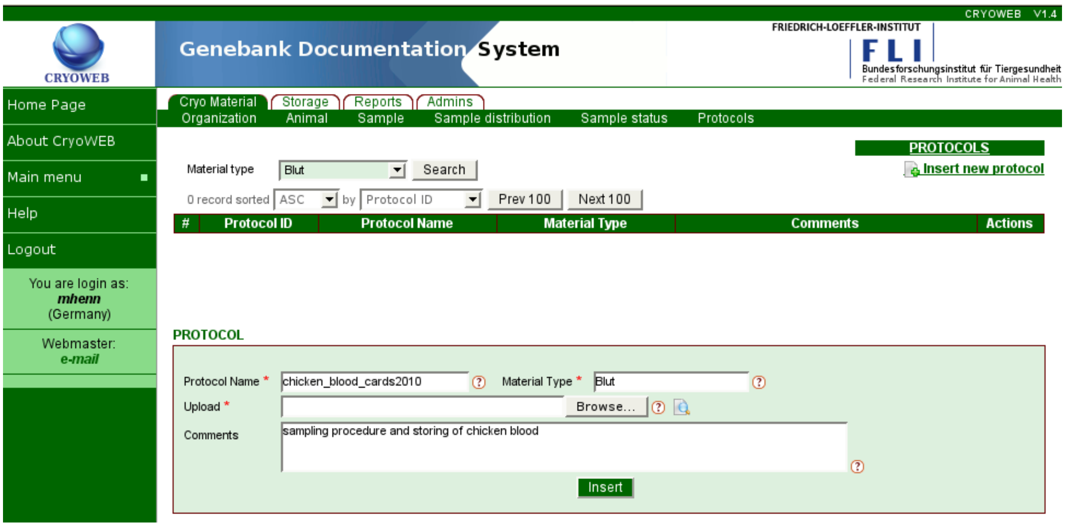
Then you should check your login and password and try again.

7.2 Protocols management

The description of each sample has to be accompanied by a clear documentation of its production/conservation procedure. The documentation for one protocol must reside in single file, OpenOffice- or Microsoft Office document, PDF file or archive. For a discussion see 6.2.8.

7.2.1 Adding new protocol

Open **Main Menu** ▷ **Cryo material** ▷ **Protocols** by clicking on the respective menu items and tabs! Choose **Material type** from the list and click the **Search** button to list all available protocols for that type. Click on the **Insert new protocol** to start entering data.



You are login as:
mhenn
(Germany)

Material type: Blut

ASC by Protocol ID

Protocol Name *: chicken_blood_cards2010

Material Type *: Blut

Upload *:

Comments: sampling procedure and storing of chicken blood

Figure 7.2: Insert new protocol

The **Material type** entry field on the form will be automatically filled with the current selection in the **Material type** drop-down list, and this value cannot be changed (Figure 7.2). The **Submit** button will change its label to **Insert**. Mandatory items (*) on this form are **Protocol name** and **Protocol file** (the **Upload** field). Enter a short and meaningful protocol name in the respective field as this name will occur in the drop-down list on the **Sample** form. To upload a protocol file, click on the **Browse** button (**Choose File** in Safari browser) and choose the file from your file system of your local computer. Keep in mind that the **Browse** button is a browser specific button and will be shown in the language of the browser. For example, if your browser is localized in German language, then the button label will be **Durchsuchen**. To enter the new protocol data in the database, click the **Insert** button. If the insert was successful, the new protocol name will show in the protocols list above the **Protocol** form.

7.2.2 Viewing protocol file

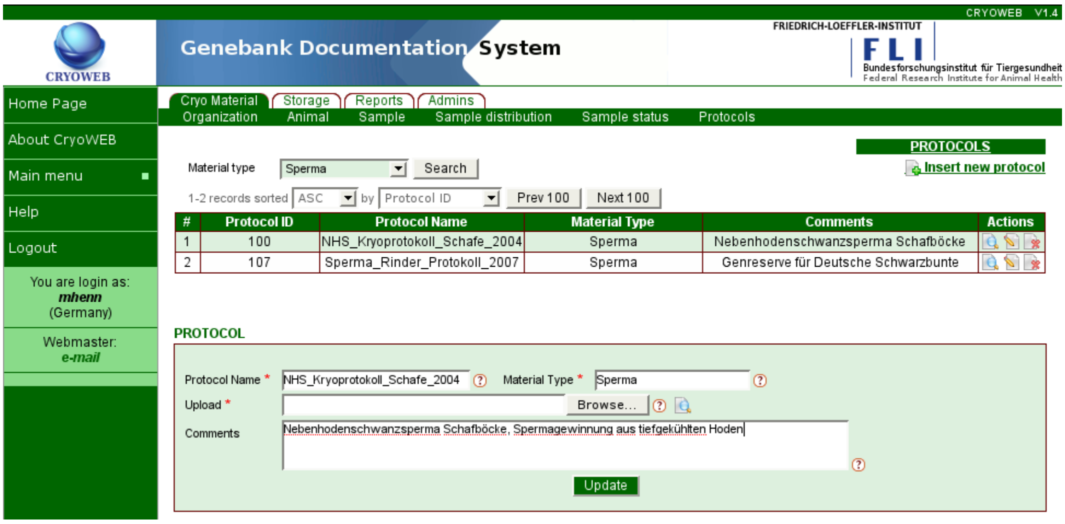
To view an attached protocol file, open the protocol page via **Main Menu** ▷ **Cryo material** ▷ **Protocols**. Choose the material type from the respective drop-down list and click the **Search** button. Find the line containing the name of the protocol and click the **View** (left) icon in the **Actions** section of this line. The protocol name, material type and comments for the protocol will be filled in the **Protocol** form below. No file name is shown in the **Upload** field, the reason for this being file names are not stored in the database. However, you can open or save the protocol file to your computer by clicking the magnifier icon next to the **Upload** field.

7.2.3 Updating protocol data

There are several options when you have to change something related to the protocol files.

To update protocol click on **Main Menu** ▷ **Cryo material** ▷ **Protocols**. Choose the material type from the respective drop-down list and click the **Search** button.

The available protocols for the chosen material type will be listed below. Find the line containing the name of the protocol you want to update, and click the **Update**(middle) icon in the **Actions** section of this line (Figure 7.3). Make the corrections in the respective form fields, e.g. change the protocol name, or upload new protocol file, and click the **Update** button in the bottom of the form to submit the changes to the database.



Material type: Sperma

1-2 records sorted ASC by Protocol ID

#	Protocol ID	Protocol Name	Material Type	Comments	Actions
1	100	NHS_Kryoprotokoll_Schafe_2004	Sperma	Nebenhodenschwanzsperma Schafböcke	
2	107	Sperma_Rinder_Protokoll_2007	Sperma	Genreserve für Deutsche Schwarzbunte	

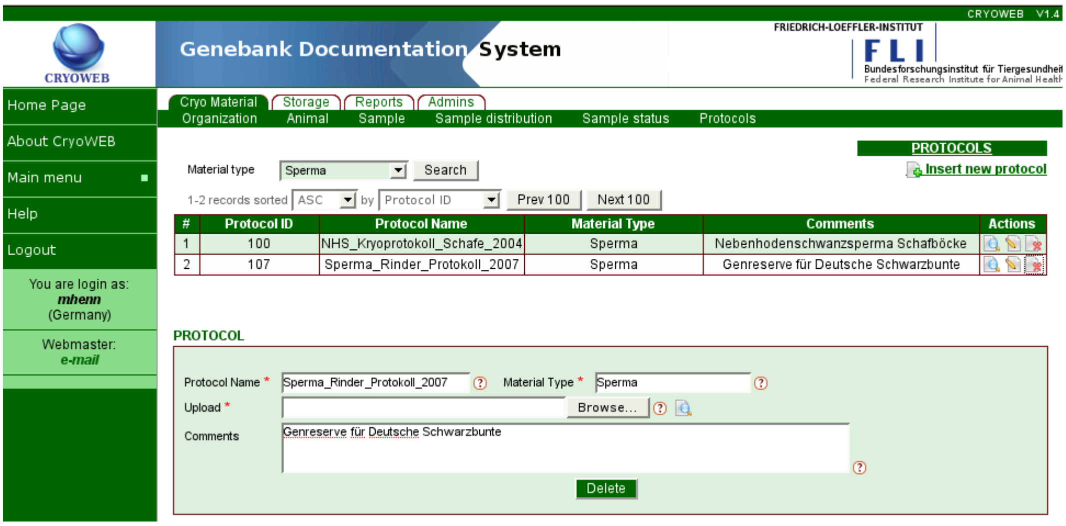
Protocol Name *: NHS_Kryoprotokoll_Schafe_2004
Material Type *: Sperma
Upload *:
Comments: Nebenhodenschwanzsperma Schafböcke, Spermagewinnung aus tiefgekühlten Hoden

Figure 7.3: Update protocol data

7.2.4 Deleting a protocol

Open the **Protocols** page via **Main Menu** ▷ **Cryo material** ▷ **Protocols**. Choose the material type from the respective drop-down list and click the **Search** button.

The protocols available for the chosen material type will be listed below. Find the line containing the name of the protocol you want to delete and click the **Delete** (right) icon in the **Actions** section of this line.



Material type: Sperma

1-2 records sorted ASC by Protocol ID

#	Protocol ID	Protocol Name	Material Type	Comments	Actions
1	100	NHS_Kryoprotokoll_Schafe_2004	Sperma	Nebenhodenschwanzsperma Schafböcke	
2	107	Sperma_Rinder_Protokoll_2007	Sperma	Genreserve für Deutsche Schwarzbunte	

Protocol Name *: Sperma_Rinder_Protokoll_2007
Material Type *: Sperma
Upload *:
Comments: Genreserve für Deutsche Schwarzbunte

Figure 7.4: Delete a protocol

The data for the protocol will be shown in the **Protocol** form below (Figure 7.4). To erase the protocol, click on the **Delete** button in the bottom of the form. A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK** (**Cancel** prevents you from deleting records by mistake).

7.3 Storage management

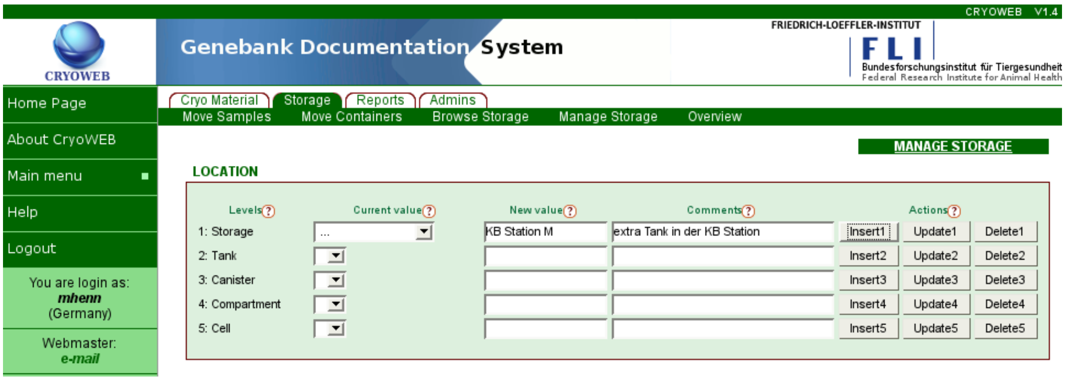
Sample locations are organized in a hierarchy of five levels. These five levels should uniquely describe the storage locations in the country and allow the user to find the samples. The first level **Storage** can be the name of the institution, where the cryo tank is kept. The second level by default is the tank, or the freezer. The third item in the hierarchy can be the canister within the tank, the forth - the level inside the canister and the fifth - the goblet. In some storage places the goblets may not have separate identification, and the levels may be organized in different manner. Therefore, each country has to have a **Policy** about the location levels.

7.3.1 Adding a new storage place

Choose **Main menu** ▷ **Storage** ▷ **Manage Storage** In the field **New value** of the line **1: Storage** fill the name of the institution or the storage place. Add comments in the **Comments** field on the same line concerning specifics of the place (Figure 7.5). Click the **Insert1** button to send the information to the database. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



You are login as: **mhenn** (Germany)

Levels	Current value	New value	Comments
1: Storage	...	KB Station M	extra Tank in der KB Station
2: Tank			
3: Canister			
4: Compartment			
5: Cell			

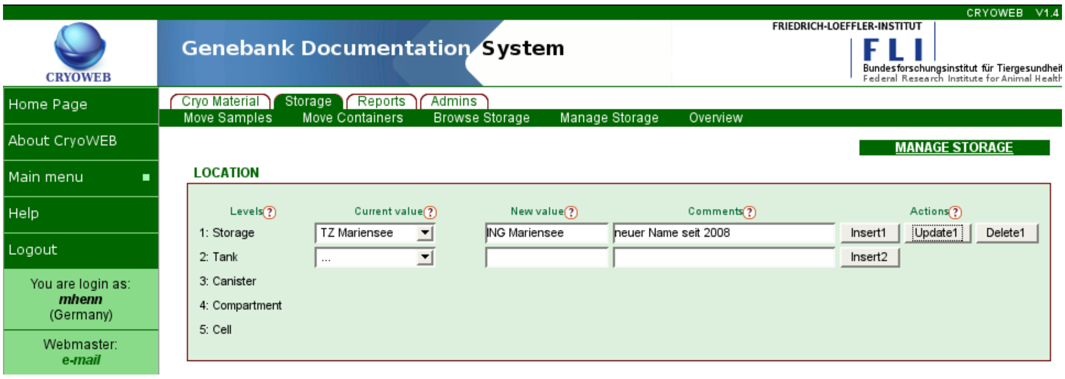
Figure 7.5: Add new storage place

7.3.2 Renaming a storage place

Open **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name you want to change. The name will be shown both in the **Current value** list selection and in the **New value** field. Change the name in the field **New value**. Add comments why this storage place has to be renamed in the **Comments** field. Click on the **Update1** button to enter the new name (Figure 7.6). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



1: Storage — Current value: TZ Mariensee; New value: ING Mariensee; Comments: neuer Name seit 2008

2: Tank — Current value: ...

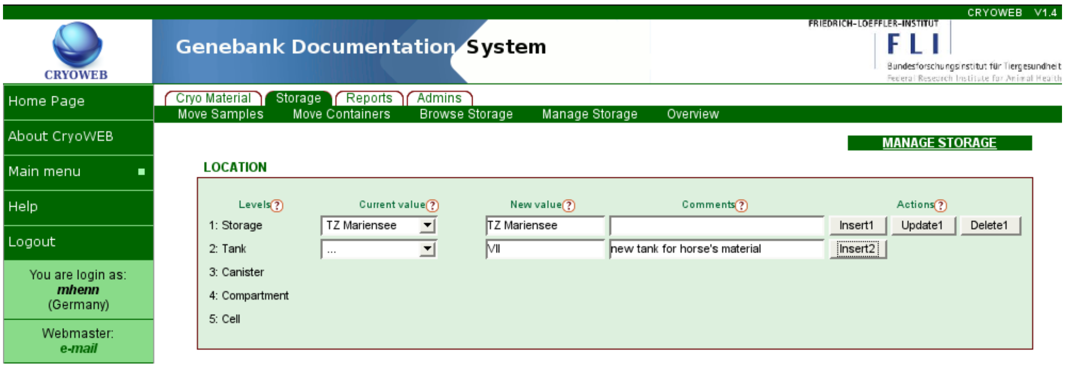
Figure 7.6: Rename a storage place

7.3.3 Adding a new tank or freezer

There is a variety of cryo tanks that differ in size and capacity. In order to list the tanks, you will have to insert their identifications as the second level in the location hierarchy. Open **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage, where this tank is located. Fill the tank identification in the field **New value** on the **2: Tank** line (Figure 7.7). Add comments, if applicable, in the **Comments** field. Use the **Insert2** button to enter the new identification in the database. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



1: Storage — Current value: TZ Mariensee; New value: TZ Mariensee

2: Tank — Current value: ...; New value: VII; Comments: new tank for horse's material

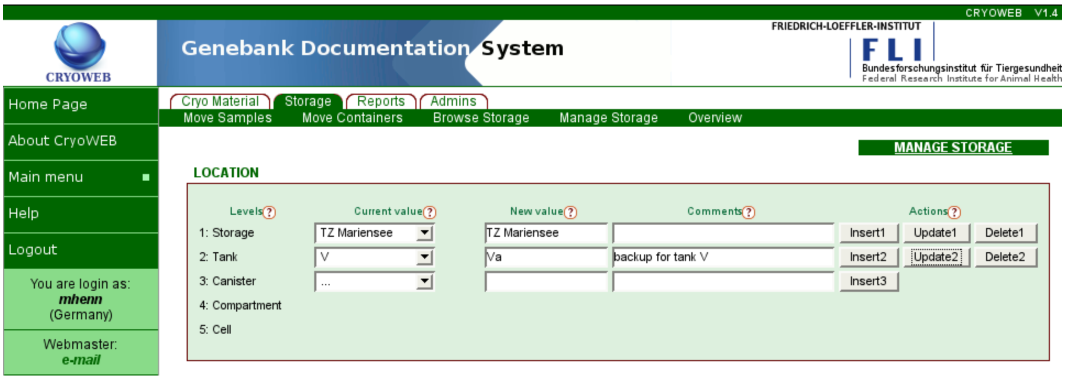
Figure 7.7: Add new tank or freezer

7.3.4 Relabeling a tank

In case a tank needs a new label (name or number) you choose **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage, where this tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank identification, you want to relabel. Change the name in the field **New value** in the line **2: Tank**. Add comments, why this tank had to be renamed in the **Comments** field on the same line. Use the **Update2** button (Figure 7.8) to enter the new name. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



Levels	Current value	New value	Comments
1: Storage	TZ Mariensee	TZ Mariensee	
2: Tank	V	Va	backup for tank V
3: Canister	...		
4: Compartment			
5: Cell			

Figure 7.8: Relabel a tank

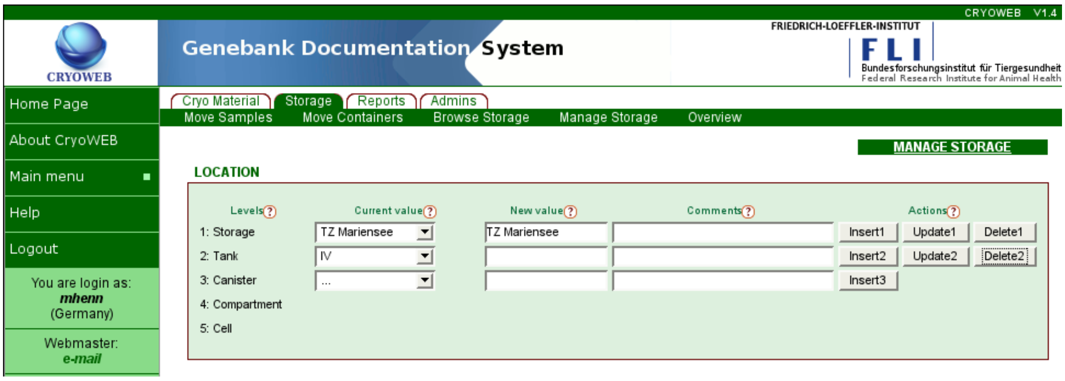
7.3.5 Deleting a tank

Open **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage, where this tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank you want to delete. Click the **Delete2** (Figure 7.9). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**! (or click **Cancel** if you are not sure you want to delete this tank).

Note: If you delete a tank, all canisters within this tank will be also deleted (along with their compartments and cells). This is only possible if there are no samples stored in this part of the location hierarchy, in all other cases you will get an error message and the tank record will remain in the database.



Levels	Current value	New value	Comments
1: Storage	TZ Mariensee	TZ Mariensee	
2: Tank	IV		
3: Canister	...		
4: Compartment			
5: Cell			

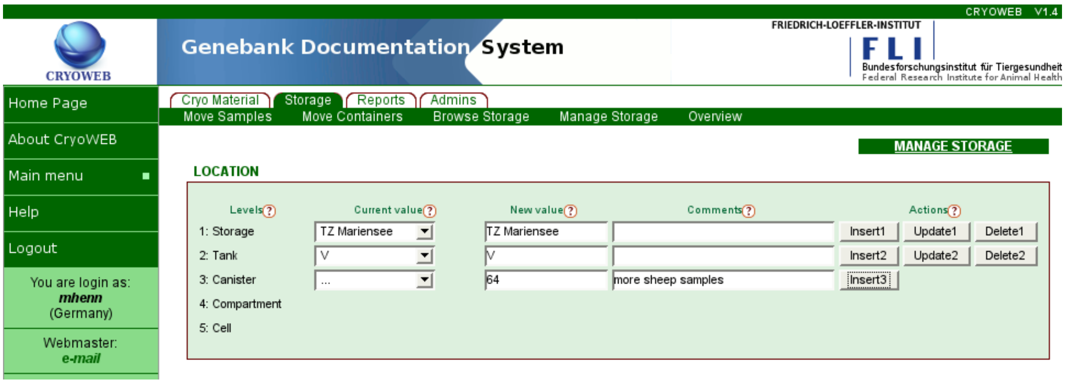
Figure 7.9: Delete a tank

7.3.6 Adding a canister in tank

Open the page **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage, where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Fill in the identification of the new canister in the field **New value** on the line **3: Canister** (Figure 7.10). Add relevant comments in the **Comments** field. Use the **Insert3** button to send the data to the database. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



Levels	Current value	New value	Comments
1: Storage	TZ Mariensee	TZ Mariensee	
2: Tank	V	V	
3: Canister	...	64	more sheep samples
4: Compartment			
5: Cell			

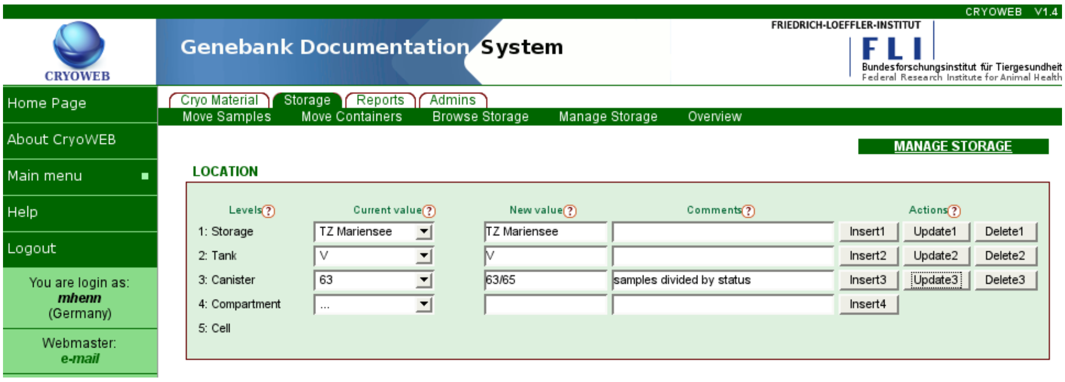
Figure 7.10: Add a canister in tank

7.3.7 Relabeling a canister

In case a canister needs a new label (name or number) choose **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Change the canister identification in the field **New value** in the same line **3: Canister**. Add comments, why this canister had to get a new label in the **Comments** field. Use the **Update3** button to update the canister identification (Figure 7.11). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



Levels?	Current value?	New value?	Comments?	Actions?		
1: Storage	TZ Mariensee	TZ Mariensee		Insert1	Update1	Delete1
2: Tank	V	V		Insert2	Update2	Delete2
3: Canister	63	63/65	samples divided by status	Insert3	Update3	Delete3
4: Compartment	...			Insert4		
5: Cell						

Figure 7.11: Relabel canister

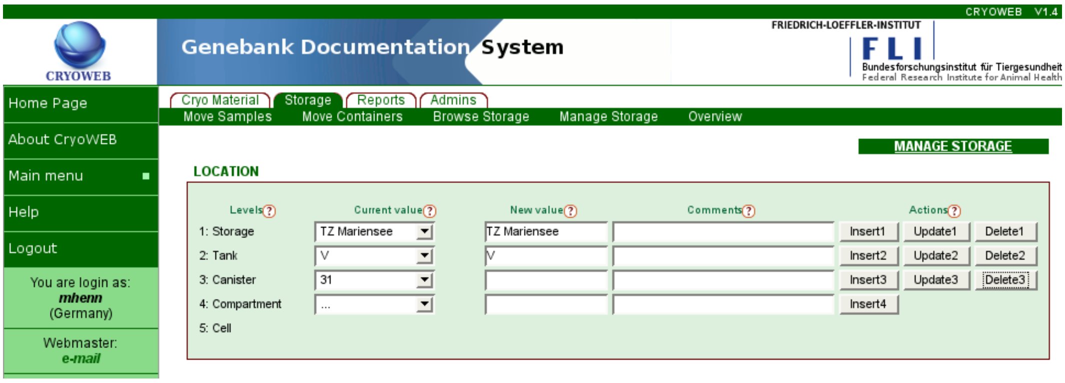
7.3.8 Deleting a canister

Open this page via **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage, where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Click the **Delete3** button (Figure 7.12). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**! (or click **Cancel** if you are not sure you want to delete this canister).

Note: If you delete a canister all its compartments and cells will be also erased. This is only possible if there are no samples stored in this part of the location hierarchy, in all other cases you will get an error message and the canister will remain.

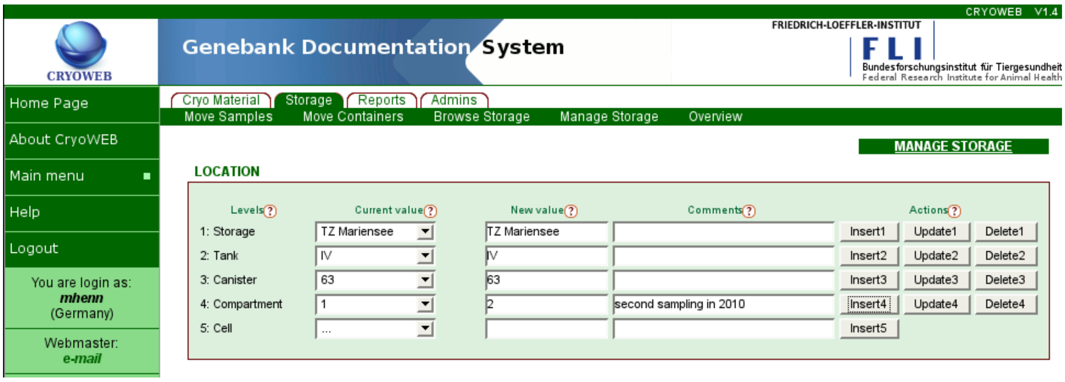


1: Storage TZ Mariensee TZ Mariensee
2: Tank V V
3: Canister 31
4: Compartment ...
5: Cell

Figure 7.12: Delete canister

7.3.9 Describing the canister levels

Canisters may have more than one level or compartment, depending on the type and size of the tank. To add a compartment to a canister, open this page **Main menu** ▷ **Storage** ▷ **Manage Storage**.



1: Storage TZ Mariensee TZ Mariensee
2: Tank IV IV
3: Canister 63 63
4: Compartment 1 2 second sampling in 2010
5: Cell ...

Figure 7.13: Describe the canister levels

Choose from the **Current value** list in the line **1: Storage** the name of the storage, where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Fill in the identification of the new compartment in the field **New value** on the line **4: Compartment**. Add relevant comments in the **Comments** field (Figure 7.13).

Use the **Insert4** button to send the data to the database. A confirmation dialog

```
Are you sure that you want to execute this action?
```

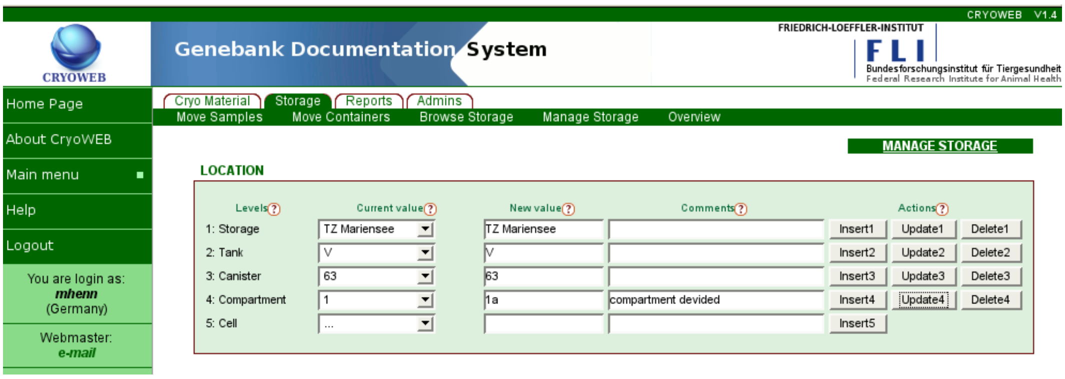
will be shown. Confirm with **OK**!

7.3.10 Relabeling compartments

In case a canister level, or compartment needs a new label (name or number) choose **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage, where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Wait until the **Current value** list in the line **4: Compartment** is populated and select the canister level (compartment). Change the compartment identification in the field **New value** in the same line **4: Compartment**. Add comments, why this compartment had to get a new label in the **Comments** field. Use the **Update4** button to update the compartment identification (Figure 7.14). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



Levels	Current value	New value	Comments	Actions		
1: Storage	TZ Mariensee	TZ Mariensee		Insert1	Update1	Delete1
2: Tank	V	V		Insert2	Update2	Delete2
3: Canister	63	63		Insert3	Update3	Delete3
4: Compartment	1	1a	compartment devided	Insert4	Update4	Delete4
5: Cell	...			Insert5		

Figure 7.14: Relabel compartment

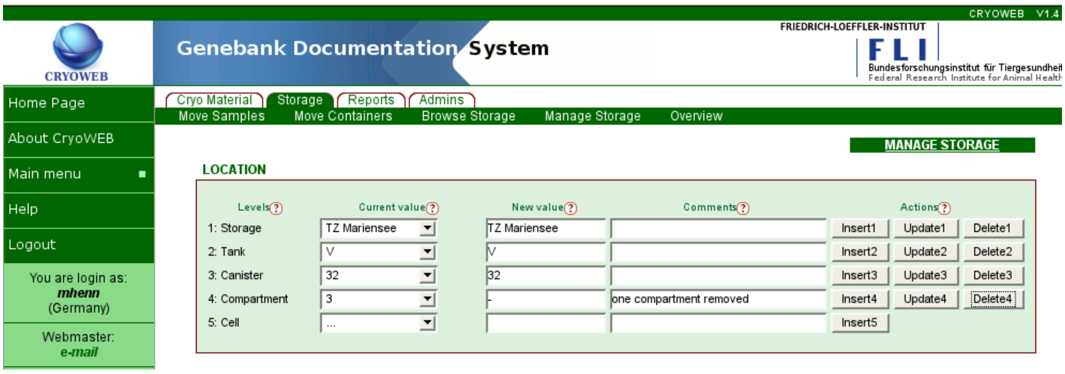
7.3.11 Deleting a compartment

Open this page via **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Wait until the **Current value** list in the line **4: Compartment** is populated and select the canister level (compartment). Click the **Delete4** button (Figure 7.15). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**! (or click **Cancel** if you are not sure you want to delete this compartment).

> **Note:** If you delete a compartment all its cells will be also erased. This is only possible if there are no samples stored in this part of the location hierarchy, in all other cases you will get an error message and the compartment will remain.



LOCATION

Levels	Current value	New value	Comments	Actions		
1: Storage	TZ Mariensee	TZ Mariensee		Insert1	Update1	Delete1
2: Tank	V	V		Insert2	Update2	Delete2
3: Canister	32	32		Insert3	Update3	Delete3
4: Compartment	3	-	one compartment removed	Insert4	Update4	Delete4
5: Cell	...			Insert5		

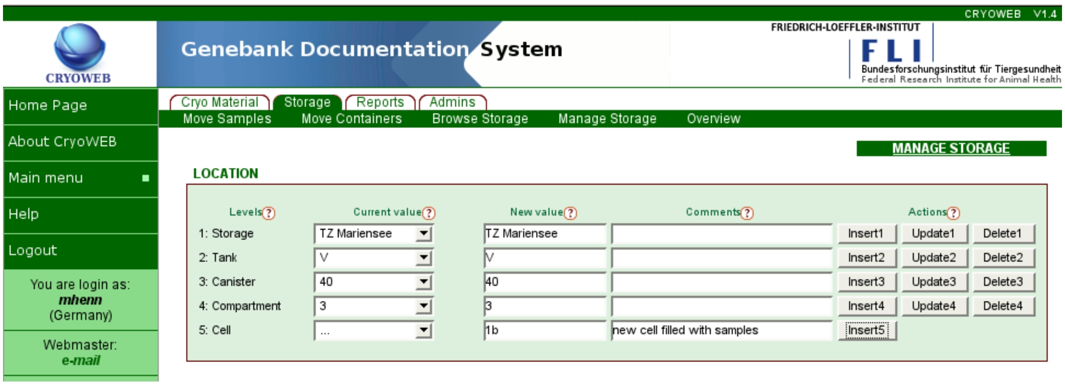
Figure 7.15: Delete compartment

7.3.12 Adding a cell in a compartment

Compartments are usually divided into cells, or smaller goblets are stored in each canister level depending on the type and size of the tank. To add a cell to a compartment, open this page **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage, where the tank is located. Wait until the **Current value** list in the line **2:Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Wait until the **Current value** list in the line **4: Compartment** is populated and select the canister level (compartment). Fill in the identification of the new cell in the field **New value** on the line **5: Cell**. Add relevant comments in the **Comments** field (Figure 7.16). Use the **Insert5** button to send the data to the database. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



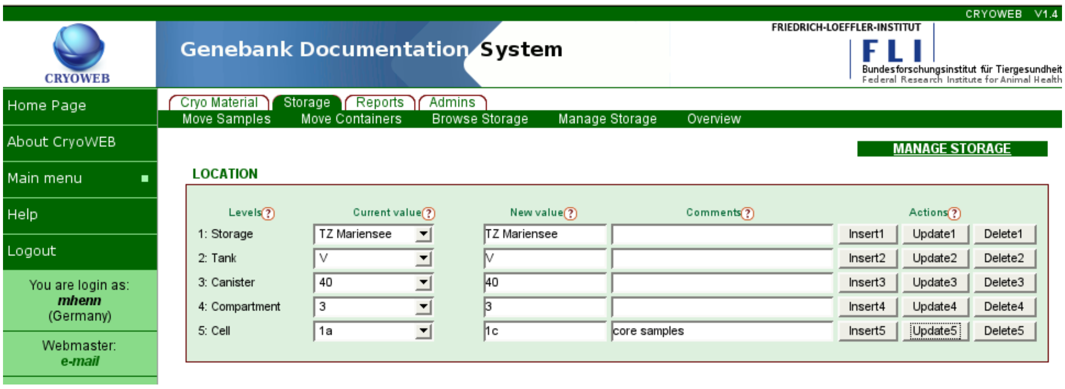
LOCATION

Levels	Current value	New value	Comments	Actions		
1: Storage	TZ Mariensee	TZ Mariensee		Insert1	Update1	Delete1
2: Tank	V	V		Insert2	Update2	Delete2
3: Canister	40	40		Insert3	Update3	Delete3
4: Compartment	3	3		Insert4	Update4	Delete4
5: Cell	...	1b	new cell filled with samples	Insert5		

Figure 7.16: Add cell in a compartment

7.3.13 Relabeling a cell

In case a cell needs a new label (name or number) choose **Main menu** ▷ **Storage** ▷ **Manage Storage**.



LOCATION

Levels	Current value	New value	Comments	Actions		
1: Storage	TZ Mariensee	TZ Mariensee		Insert1	Update1	Delete1
2: Tank	V	V		Insert2	Update2	Delete2
3: Canister	40	40		Insert3	Update3	Delete3
4: Compartment	3	3		Insert4	Update4	Delete4
5: Cell	1a	1c	core samples	Insert5	Update5	Delete5

Figure 7.17: Relabel cell

Choose from the **Current value** list in the line **1: Storage** the name of the storage where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Wait until the **Current value** list in the line **4: Compartment** is populated and select the canister level (compartment). Wait until the **Current value** list in the line **5: Cell** is populated and select the cell. Change the cell identification in the field **New value** in the same line **5: Cell**. Add comments, why this cell had to get a new label in the **Comments** field. Use the **Update5** button to update the cell identification (Figure 7.17). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

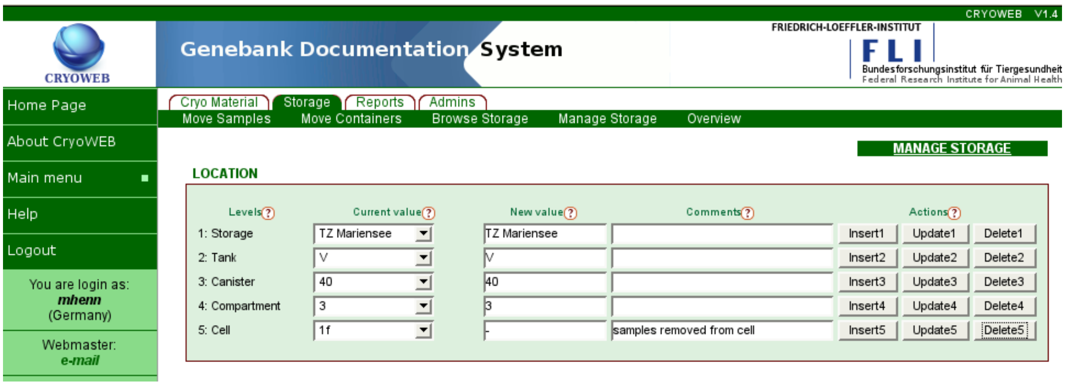
7.3.14 Deleting a cell

Open this page via **Main menu** ▷ **Storage** ▷ **Manage Storage**. Choose from the **Current value** list in the line **1: Storage** the name of the storage where the tank is located. Wait until the **Current value** list in the line **2: Tank** is populated and select the tank. Wait until the **Current value** list in the line **3: Canister** is populated and select the canister. Wait until the **Current value** list in the line **4: Compartment** is populated and select the canister level (compartment). Wait until the **Current value** list in the line **5: Cell** is populated and select the cell.Click the **Delete5** button (Figure 7.18). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**! (or click **Cancel** if you are not sure you want to delete this cell).

> **Note:** Deletion of a cell is only possible if there are no samples stored in this part of the location hierarchy, in all other cases you will get an error message and the cell will remain.



Levels	Current value	New value	Comments	Actions		
1: Storage	TZ Mariensee	TZ Mariensee		Insert1	Update1	Delete1
2: Tank	V	V		Insert2	Update2	Delete2
3: Canister	40	40		Insert3	Update3	Delete3
4: Compartment	3	3		Insert4	Update4	Delete4
5: Cell	1f	-	samples removed from cell	Insert5	Update5	Delete5

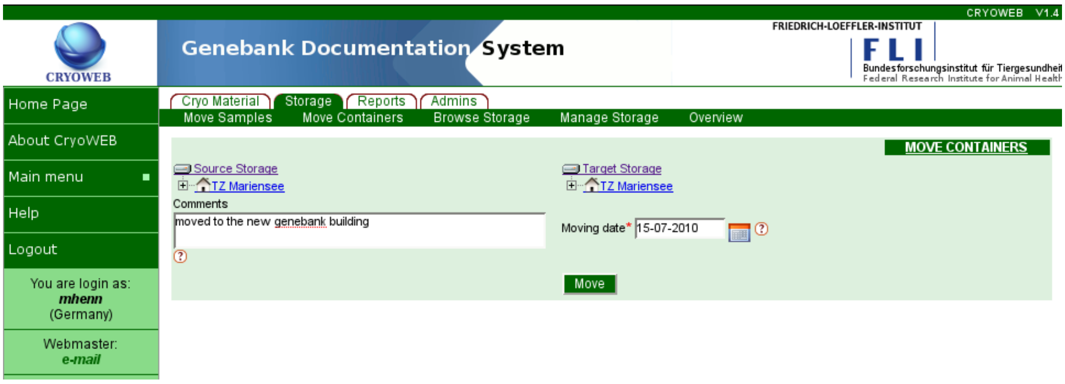
Figure 7.18: Delete cell

7.3.15 Moving a tank to a different location

Sometimes entire tanks with all their content have to be moved to a different location. For recording such movement open **Main menu** ▷ **Storage** ▷ **Move Containers**.

Two hierarchy trees are shown on the form - **Source Storage** and **Target Storage**. **Source Storage** is the location where the container comes from, **Target Storage** where the container goes to (Figure 7.19).

Click on the + sign before the name of the storage, where the tank was originally located in the **Source Storage** to expand the hierarchy tree. Mark the tank by clicking on its identification. Then click the name of the storage where the tank was moved to in the **Target Storage** tree. Fill in the **Comments** field the reasons for the movement. Fill the date of the movement by picking from the respective calendar control. The **Moving date** is a mandatory field. Click **Move** and the movement is immediately recorded in the database.



Comments: moved to the new genebank building

Moving date*: 15-07-2010

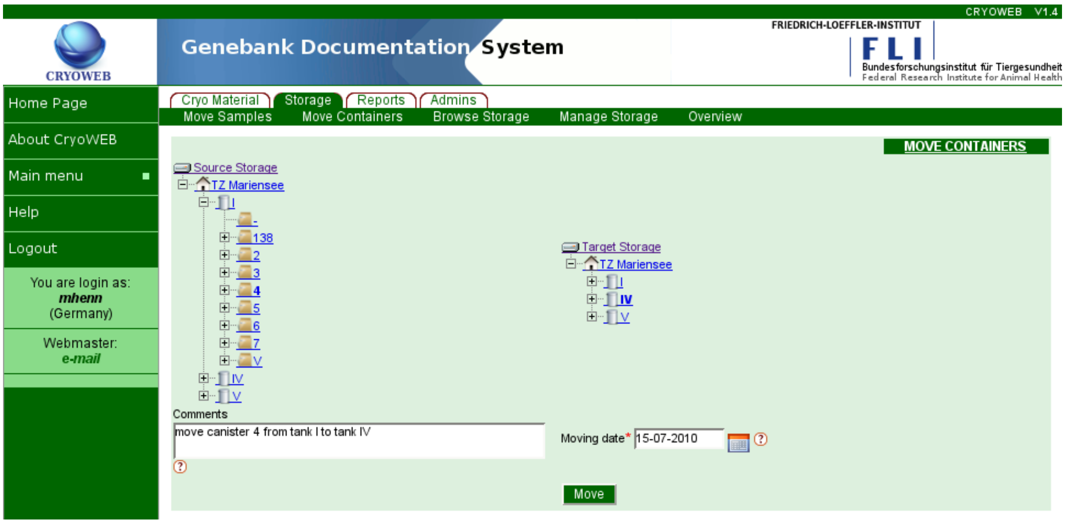
Figure 7.19: Move tank to a different location

7.3.16 Moving a canister to a different tank

Canisters may be moved from one tank to another (in case it is the same model of tank). Open the pages **Main menu** ▷ **Storage** ▷ **Move Containers**.

In the **Source Storage** click on the + sign before the name of the storage, where the canister was originally located to expand the hierarchy tree. Then click on the + sign before the name of the tank, where the canister was originally located. Mark the canister to be moved by clicking on its identification. In the **Target Storage** click on the + sign before the name of the storage, where the canister will be moved to. Then click on the + sign before the identification of the tank where the canister will be moved. Fill in the **Comments** field the reason for the movement. Fill the **Moving date** field by picking date from the respective calendar control. Click **Move** to record the changes in the database (Figure 7.20).

Note: The canister can be moved only in a tank. If you try to move the canister to another level, e.g. directly in a storage, an error message will be shown and the movement is refused.



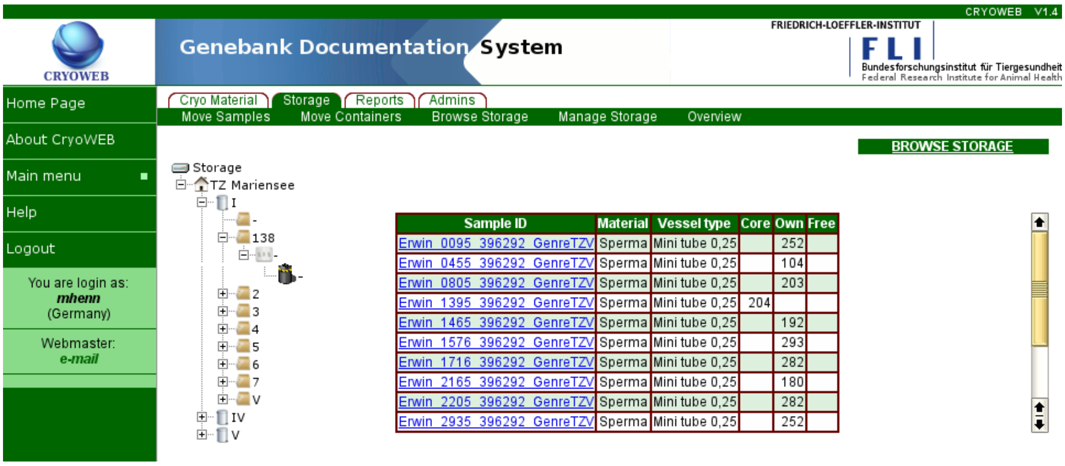
Comments: move canister 4 from tank I to tank IV

Moving date*: 15-07-2010

Figure 7.20: Move canister in different location

7.3.17 Browsing the genebank storage

The option **Browse storage** allows the user to navigate through the storage locations hierarchy and see its content. Open **Main menu** ▷ **Storage** ▷ **Browse Storage** (Figure 7.21).



Sample ID	Material	Vessel type	Core	Own	Free
Erwin_0095_396292_GenreTZV	Sperma	Mini tube 0,25		252	
Erwin_0455_396292_GenreTZV	Sperma	Mini tube 0,25		104	
Erwin_0805_396292_GenreTZV	Sperma	Mini tube 0,25		203	
Erwin_1395_396292_GenreTZV	Sperma	Mini tube 0,25	204		
Erwin_1465_396292_GenreTZV	Sperma	Mini tube 0,25		192	
Erwin_1576_396292_GenreTZV	Sperma	Mini tube 0,25		293	
Erwin_1716_396292_GenreTZV	Sperma	Mini tube 0,25		282	
Erwin_2165_396292_GenreTZV	Sperma	Mini tube 0,25		180	
Erwin_2205_396292_GenreTZV	Sperma	Mini tube 0,25		282	
Erwin_2935_396292_GenreTZV	Sperma	Mini tube 0,25		252	

Figure 7.21: Browsing the genebank storage

Expand the tree by clicking on the + sign before the name of the storage, then click the + before the identification of the tank and continue in the same manner with the canister and compartment. If there are any cells (goblets) in this compartment, they will be shown now on the screen. To see the content of a cell, click on its identification in the tree. A list of all samples stored in that cell will be shown on the right. The list contains the sample identification, type of material, type of the storage vessel and the legal status of the material.

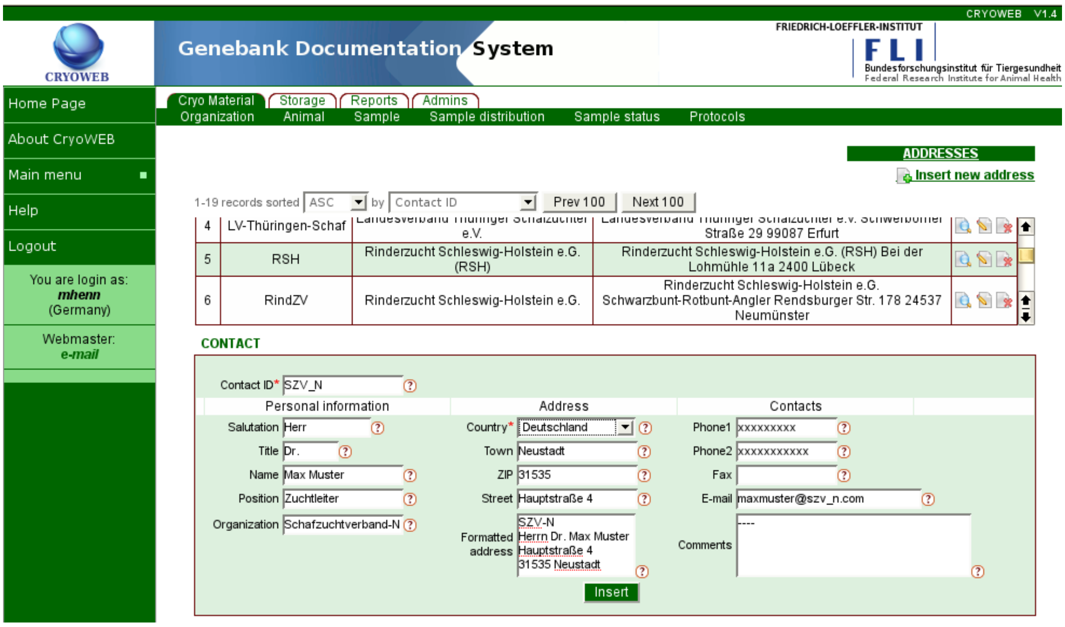
To see more details about a sample, position and hold the mouse pointer over the **Sample ID**. The system will show details about the animal donor and all the locations containing parts of this sample.

7.4 Contacts management

The CryoWEB software allows you to create a contacts repository of organizations and persons involved with the national genebank. Moreover, for each donor, one of the mandatory data items is the contact organization, which can provide more information about this animal. Before inserting a new donor in CryoWEB, you have to enter the data for the respective organization.

7.4.1 Adding a new organization

Open **Main Menu** ▹ **Cryo material** ▹ **Organization**. Click on the **Insert new address** to start entering data. The **Submit** button will change its label to **Insert**. The mandatory fields on this form are the **Contact ID** and the **Country**. The **Contact ID** must be a unique short identifier of the organization (or the person), which will be shown in drop-down lists on other forms.



1-19 records sorted ASC by Contact ID

4	LV-Thüringen-Schaf	Landesverband Thüringer Schafzüchter e.V.	Landesverband Thüringer Schafzüchter e.V. Schwerborner Straße 29 99087 Erfurt
5	RSH	Rinderzucht Schleswig-Holstein e.G. (RSH)	Rinderzucht Schleswig-Holstein e.G. (RSH) Bei der Lohmühle 11a 2400 Lübeck
6	RindZV	Rinderzucht Schleswig-Holstein e.G.	Rinderzucht Schleswig-Holstein e.G. Schwarzbunt-Rotbunt-Angler Rendsburger Str. 178 24537 Neumünster

Contact ID* SZV_N
Salutation Herr
Title Dr.
Name Max Muster
Position Zuchtleiter
Organization Schafzuchtverband-N
Country* Deutschland
Town Neustadt
ZIP 31535
Street Hauptstraße 4
Formatted address SZV-N
Herrn Dr. Max Muster
Hauptstraße 4
31535 Neustadt
Phone1 xxxxxxxxx
Phone2 xxxxxxxxxxx
Fax
E-mail maxmuster@szv_n.com
Comments ----

Figure 7.22: Add new organization

The form is logically divided in three blocks - **Personal information**, **Address** and **Contacts**. Enter in the left column (**Personal information**) fields the salutation, title and the full name of a contact person for this organization, along with his/her position within the organization (Figure 7.22). Note: it is advisable to enter the name in the order surname, given name for easy searching later on.

In the middle column (**Address**) fields enter the address of the organization, starting with country. In the special field **Formatted address** type the complete address of the organization, the way it should be printed on a envelop label.

In the fields in the right column (**Contacts**) enter the contact phones, fax, email of the organization. The field comments is for any additional information you might find suitable for recording for this organization.

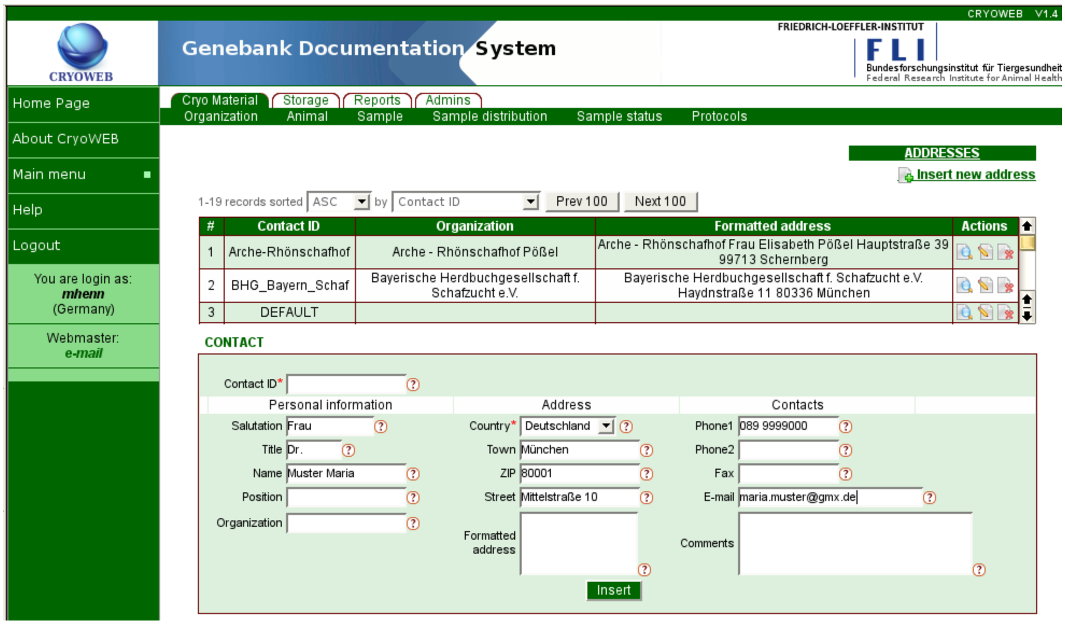
To enter the new organization in the database click the **Insert** button. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

7.4.2 Adding a new person

The procedure for registering a person in the contacts database is very similar to the one for organization, described in 7.4.1. Open **Main Menu** ▷ **Cryo material** ▷ **Organization** and click on the **Insert new address**.



1-19 records sorted ASC by Contact ID

#	Contact ID	Organization	Formatted address	Actions
1	Arche-Rhönschafhof	Arche - Rhönschafhof Pößel	Arche - Rhönschafhof Frau Elisabeth Pößel Hauptstraße 39 99713 Schernberg	
2	BHG_Bayern_Schaf	Bayerische Herdbuchgesellschaft f. Schafzucht e.V.	Bayerische Herdbuchgesellschaft f. Schafzucht e.V. Haydnstraße 11 80336 München	
3	DEFAULT			

Contact ID*

Personal information
Salutation: Frau
Title: Dr.
Name: Muster Maria
Position:
Organization:

Address
Country*: Deutschland
Town: München
ZIP: 80001
Street: Mittelstraße 10
Formatted address:

Contacts
Phone1: 089 9999000
Phone2:
Fax:
E-mail: maria.muster@gmx.de
Comments:

Figure 7.23: Add new person

Enter a meaningful **unique Contact ID** for the person. Then fill the salutation, title and full name in the respective fields in the **Personal information** column. Leave the **Position** and **Organization** fields empty. Enter the person's address details in the **Address** column fields, and the contact details (phones, fax, email) in the **Contacts** column fields (Figure 7.23).

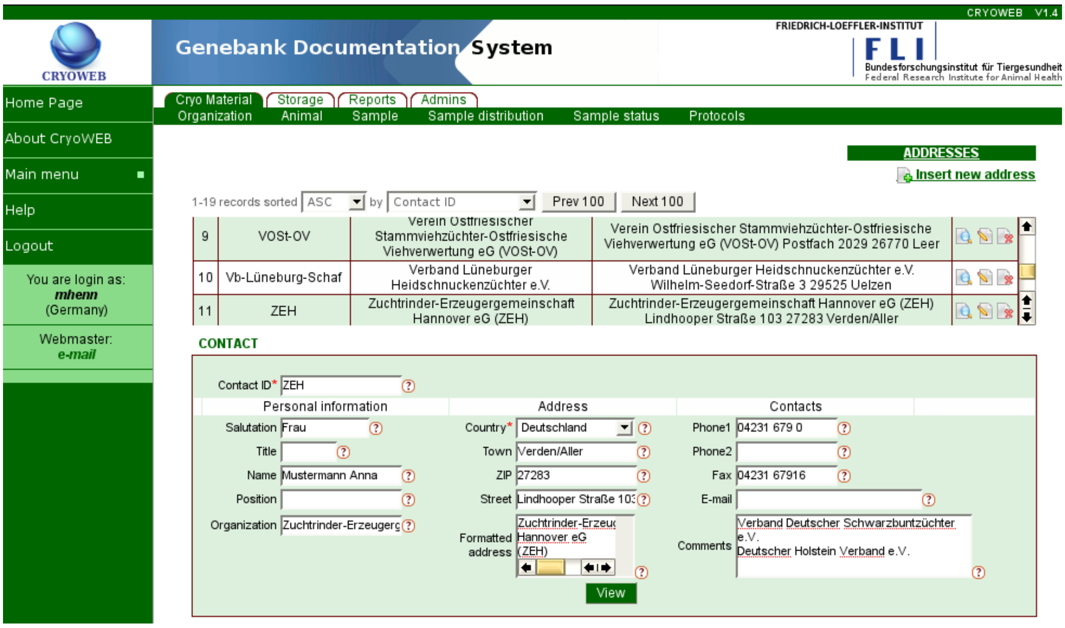
To enter the new contact record in the database click the **Insert** button. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

7.4.3 Viewing contact data

Open **Main Menu** ▷ **Cryo material** ▷ **Organization**.



1-19 records sorted ASC by Contact ID

9	VOSt-OV	Verein Ostfriesischer Stammviehzüchter-Ostfriesische Viehverwertung eG (VOSt-OV)	Verein Ostfriesischer Stammviehzüchter-Ostfriesische Viehverwertung eG (VOSt-OV) Postfach 2029 26770 Leer
10	Vb-Lüneburg-Schaf	Verband Lüneburger Heidschnuckenzüchter e.V.	Verband Lüneburger Heidschnuckenzüchter e.V. Wilhelm-Seedorf-Straße 3 29525 Uelzen
11	ZEH	Zuchtrinder-Erzeugergemeinschaft Hannover eG (ZEH)	Zuchtrinder-Erzeugergemeinschaft Hannover eG (ZEH) Lindhooper Straße 103 27283 Verden/Aller

Contact ID* ZEH

Personal information		Address		Contacts	
Salutation	Frau	Country*	Deutschland	Phone1	04231 679 0
Title		Town	Verden/Aller	Phone2	
Name	Mustermann Anna	ZIP	27283	Fax	04231 67916
Position		Street	Lindhooper Straße 10:	E-mail	
Organization	Zuchtrinder-Erzeugerg	Formatted address	Zuchtrinder-Erzeu Hannover eG (ZEH)	Comments	Verband Deutscher Schwarzbuntzüchter e.V. Deutscher Holstein Verband e.V.

Figure 7.24: View contact data

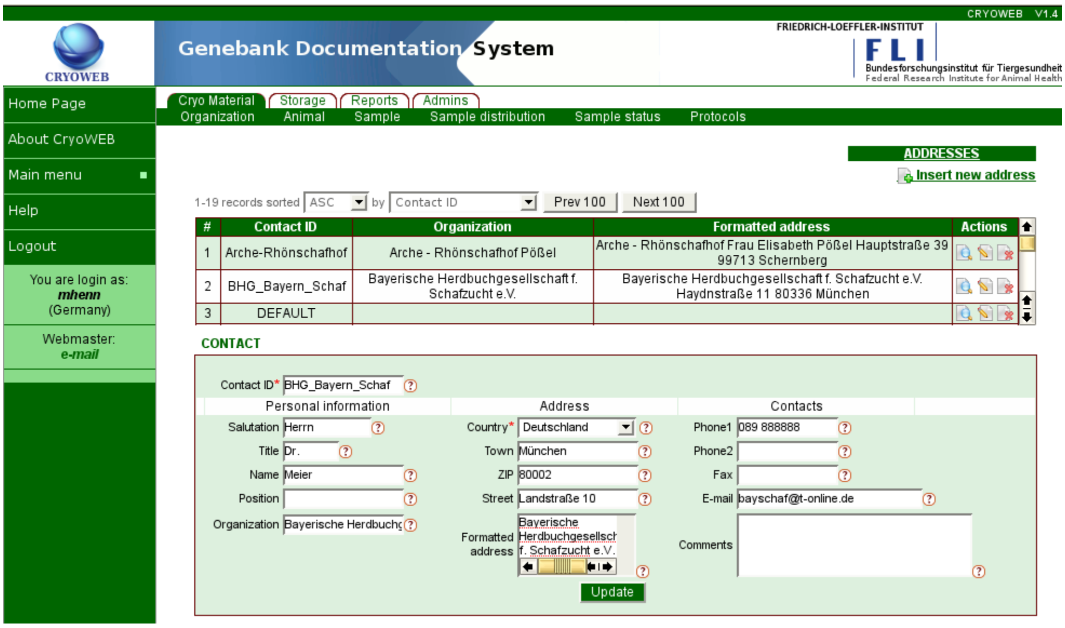
Summaries of all contact records (organizations and persons) are shown in the search result table in groups of 100. These summaries include the Contact ID, organization name and the formatted address of the contact. To view the complete data for a certain contact, navigate through the table of contacts (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the **Contact ID** you are looking for. Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The contact details will be shown in the **Contact** form below (Figure 7.24).

7.4.4 Updating contact data

To update person or organization data, click **Main Menu** ▷ **Cryo material** ▷ **Organization**, then find the line with Contact ID of the organization (person) you want to change and click the **Update** (middle) icon in the **Actions** section of this line. The submit button label will change to **Update** (Figure 7.25). Overwrite the data with the latest changes and send them to the database by clicking the **Update** button. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



1-19 records sorted ASC by Contact ID

#	Contact ID	Organization	Formatted address	Actions
1	Arche-Rhönschafhof	Arche - Rhönschafhof Pößel	Arche - Rhönschafhof Frau Elisabeth Pößel Hauptstraße 39 99713 Schernberg	
2	BHG_Bayern_Schaf	Bayerische Herdbuchgesellschaft f. Schafzucht e.V.	Bayerische Herdbuchgesellschaft f. Schafzucht e.V. Haydnstraße 11 80336 München	
3	DEFAULT			

CONTACT

Contact ID* BHG_Bayern_Schaf

Personal information		Address		Contacts	
Salutation	Herrn	Country*	Deutschland	Phone1	089 888888
Title	Dr.	Town	München	Phone2	
Name	Meier	ZIP	80002	Fax	
Position		Street	Landstraße 10	E-mail	bayschaf@t-online.de
Organization	Bayerische Herdbuchg	Formatted address	Bayerische Herdbuchgesellsch f. Schafzucht e.V.	Comments	

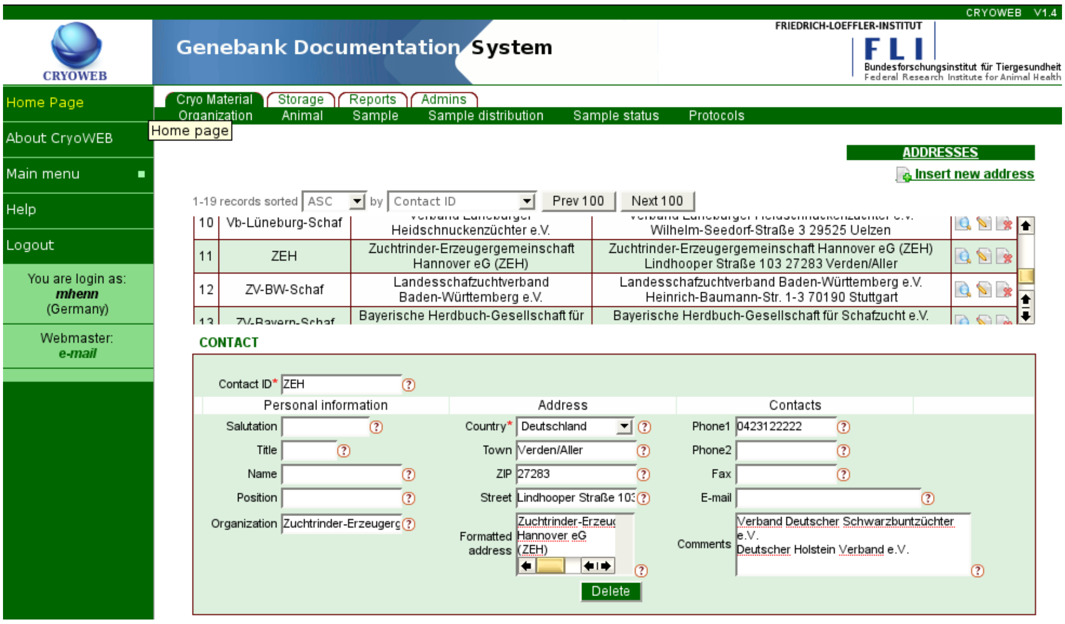
Figure 7.25: Update contact data

7.4.5 Deleting a contact

Open **Main Menu** ▷ **Cryo material** ▷ **Organization**. Navigate through the list of contacts by scrolling the contact groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself with the scroller on its right. Find in the search results the line containing the organization or person you want to delete, and click the **Delete** (right) icon in the **Actions** section of this line. The submit button label will change to **Delete** (Figure 7.26). Click then the **Delete** button, a confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**!



You are login as: **mhenn** (Germany)

Webmaster: e-mail

1-19 records sorted ASC by Contact ID

10	Vb-Lüneburg-Schaf	Heidschnuckenzüchter e.V.	Wilhelm-Seedorf-Straße 3 29525 Uelzen
11	ZEH	Zuchtrinder-Erzeugergemeinschaft Hannover eG (ZEH)	Zuchtrinder-Erzeugergemeinschaft Hannover eG (ZEH) Lindhooper Straße 103 27283 Verden/Aller
12	ZV-BW-Schaf	Landesschafzuchtverband Baden-Württemberg e.V.	Landesschafzuchtverband Baden-Württemberg e.V. Heinrich-Baumann-Str. 1-3 70190 Stuttgart
13	ZV-Bayern-Schaf	Bayerische Herdbuch-Gesellschaft für	Bayerische Herdbuch-Gesellschaft für Schafzucht e.V.

CONTACT

Contact ID* ZEH

Personal information		Address		Contacts	
Salutation		Country*	Deutschland	Phone1	0423122222
Title		Town	Verden/Aller	Phone2	
Name		ZIP	27283	Fax	
Position		Street	Lindhooper Straße 10:	E-mail	
Organization	Zuchtrinder-Erzeugerg	Formatted address	Zuchtrinder-Erzeu Hannover eG (ZEH)	Comments	Verband Deutscher Schwarzbuntzüchter e.V. Deutscher Holstein Verband e.V.

Figure 7.26: Delete contact data

7.5 Animal management

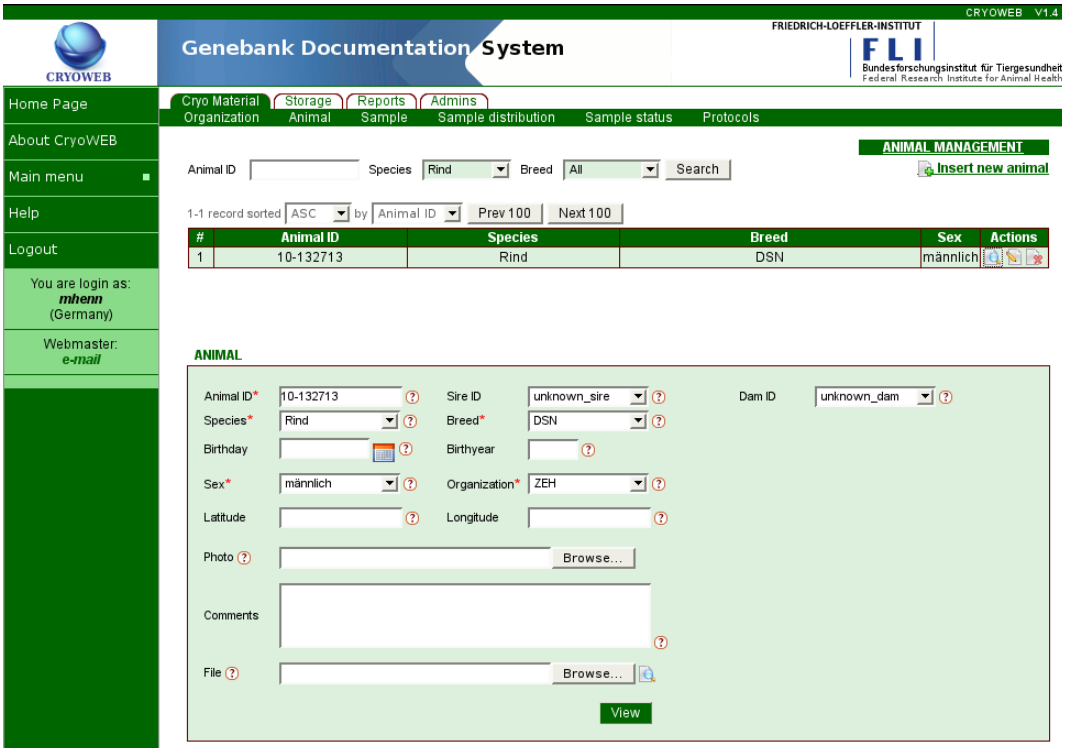
Before inserting new samples into the database, you must register its donor. In this chapter you will learn, how to add a new animal (and its pedigree) to the database, how to update the animal data, erase an animal, or add unlimited amount of data for an animal.

7.5.1 Checking if an animal is already in the database

On entering a new animal, its sire and dam must already be registered in the database, i.e. they should already have been entered as animals. Thus, before entering an animal you have to check, if the sire and the dam exist as animals in CryoWEB. Moreover, you should check, if the animal itself is not already in the database.

Open **Main Menu** ▷ **Cryo Material** ▷ **Animal**. Type the **ID** of the animal in question in the respective field in the search part. Click the **Search** button. If an animal with such identification is present in the database, it will be listed below.

If you are not sure about the correct spelling of the animal identification, type the first characters only of the **ID** and choose species and/or breed from the drop-down lists. Click on **Search** and browse through the results list to identify, if the animal is already recorded (Figure 7.27).



You are login as:
mhenn
(Germany)

Animal ID:
Species: Rind
Breed: All

1-1 record sorted ASC by Animal ID

#	Animal ID	Species	Breed	Sex	Actions
1	10-132713	Rind	DSN	männlich	

Animal ID*: 10-132713
Sire ID: unknown_sire
Dam ID: unknown_dam
Species*: Rind
Breed*: DSN
Birthday:
Birthyear:
Sex*: männlich
Organization*: ZEH
Latitude:
Longitude:
Photo:
Comments:
File:

Figure 7.27: Search for an animal ID

7.5.2 Adding a new animal

Open **Main Menu** ▷ **Cryo Material** ▷ **Animal**. Click on the **Insert_new_animal** (right side of the page) to start entering data. The submit button of the **Animal** form will change its label to **Insert**(Figure 7.28).

Fill in an unique **Animal ID**, then choose the species from the respective list. Wait until the **Breed**, **Sire ID** and **Dam ID** lists are filled with the values relevant to the chosen species and then select the donor's breed, sire and dam.

If available, fill in the animal's birth date in the **Birthday** field, if not, fill in the birth year in the respective year field. You should fill in only one of these fields or leave both empty.

Continue with coordinates of the location where the animal lives (or lived) into the fields **Latitude** and **Longitude**. The coordinates have to be in EPSG:4326 projection, without the symbol for degrees (°).

Choose (by clicking the **Browse** button near **Photo** field) an image file from your computer with a meaningful photograph of the animal (preferably with a measuring rod to indicate the size) to be uploaded with the animal data. Additional information is welcome in the **Comments** field.

If you have other files (PDF documents related to the animal like breeding or/and health certificate), put them together in an archive on your computer and select this archive for uploading in the **File**. To enter the new animal in the database click the **Insert** button. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

Animal ID | Species: All | Breed: All

1-100 records sorted ASC by Animal ID

#	Animal ID	Species	Breed	Sex	Actions
1	01-07167557	Rind	DSN	weiblich	
2	01-07167598	Rind	DSN	weiblich	
3	01-07455265	Rind	DSN	weiblich	
4	01-07455337	Rind	DSN	weiblich	

ANIMAL

Animal ID*: 11-336933
Sire ID: 10-105499
Dam ID: 01-07167557
Species*: Rind
Breed*: DSN
Birthday:
Birthyear: 1998
Sex*: männlich
Organization*: RindZV
Latitude: 51.32803
Longitude: 9.56878
Photo:
Comments: samples donated
File:

Figure 7.28: Add new animal

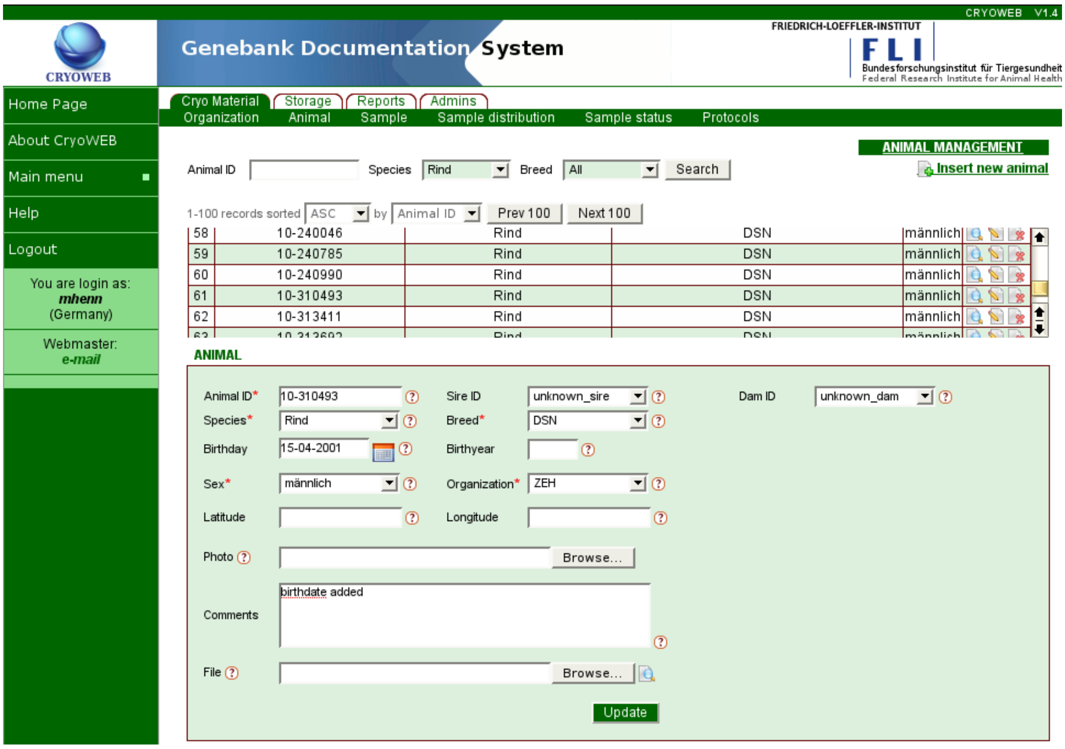
7.5.3 Updating an animal data

Open **Main Menu** ▷ **Cryo Material** ▷ **Animal**. Enter the **Animal ID** (or several starting characters of the ID only) into the first field of the search part. Click the **Search** button.

In the results list find the line containing the animal in question and click the **Update** (middle) icon in the **Actions** section of this line. The submit button label should change to **Update**. Overwrite the data with the latest changes and send them to the database by clicking the **Update** button (Figure 7.29). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!



Animal ID | Species: Rind | Breed: All

1-100 records sorted ASC by Animal ID

58	10-240046	Rind	DSN	männlich
59	10-240785	Rind	DSN	männlich
60	10-240990	Rind	DSN	männlich
61	10-310493	Rind	DSN	männlich
62	10-313411	Rind	DSN	männlich

Animal ID*: 10-310493
Sire ID: unknown_sire
Dam ID: unknown_dam
Species*: Rind
Breed*: DSN
Birthday: 15-04-2001
Birthyear:
Sex*: männlich
Organization*: ZEH
Latitude:
Longitude:
Photo:
Comments: birthdate added
File:

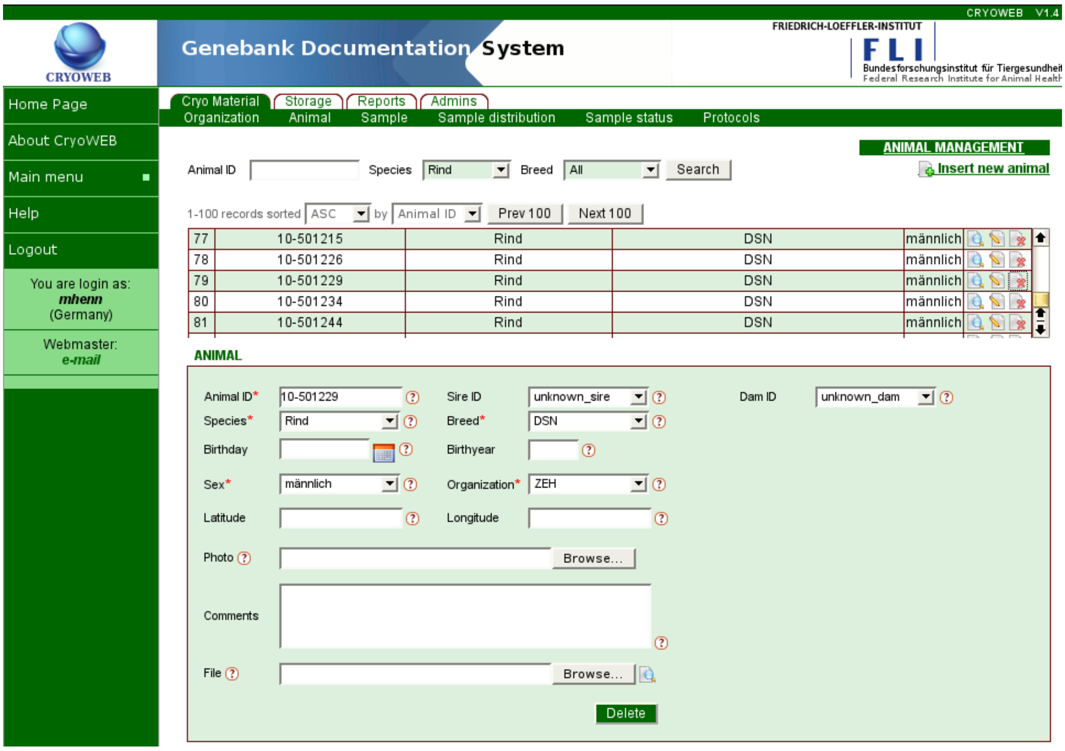
Figure 7.29: Update animal data

7.5.4 Deleting animal

Open **Main Menu** ▷ **Cryo Material** ▷ **Animal**. Enter the **Animal ID** into the first field of the search part of the page. Click the **Search** button. Find in the search results the line containing the animal you want to delete, and click the **Delete** (right) icon in the **Actions** section of this line. The submit button label should change to **Delete** (Figure 7.30). Click then the **Delete** button, a confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**!



Animal ID Species: Rind Breed: All

1-100 records sorted ASC by Animal ID

77	10-501215	Rind	DSN	männlich
78	10-501226	Rind	DSN	männlich
79	10-501229	Rind	DSN	männlich
80	10-501234	Rind	DSN	männlich
81	10-501244	Rind	DSN	männlich

Animal ID*: 10-501229
Species*: Rind
Birthday:
Sex*: männlich
Latitude:
Photo:
Comments:
File:
Sire ID: unknown_sire
Breed*: DSN
Birthyear:
Organization*: ZEH
Longitude:
Dam ID: unknown_dam

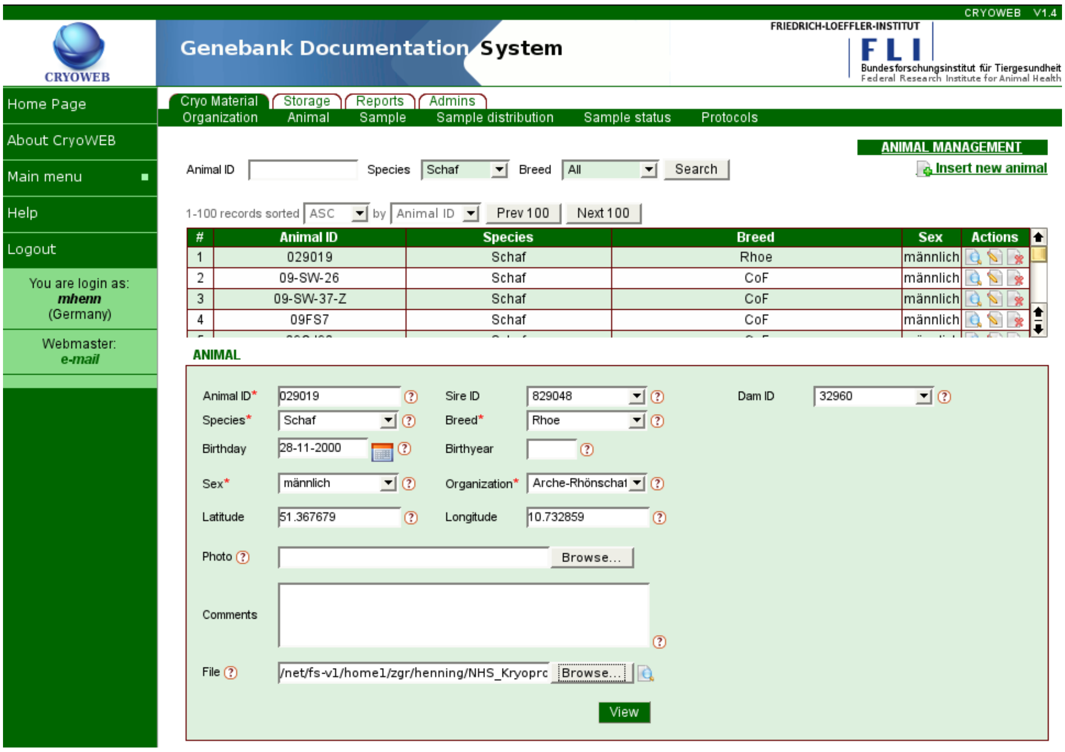
Figure 7.30: Delete animal data

7.5.5 Adding more than one file to the animal

The system allows only one image file (**Photo**) or one archive with additional documents (**File**), which have to be imported into the database. In case you want to add another file to the archive, you have to export the current archive from the web page to your local machine.

To export the archive open **Main Menu** ▷ **Cryo Material** ▷ **Animal**. Enter the **Animal ID** into the first field of the search part of the page. Click on the **Search** button. In the results list find the line containing the animal in question and click the **View** (left) icon in the Actions section of this line. The animal data will be shown in the form below. Click the magnifier near the **File** field to open/export the archive.

On your computer, add the new file to the archive using the respective archive manager software (e.g. **Ark**, **WinRar**).Then upload again the archive following the procedure for updating animal data (Figure 7.31).



Animal ID Species Schaf Breed All

1-100 records sorted ASC by Animal ID

#	Animal ID	Species	Breed	Sex	Actions
1	029019	Schaf	Rhoe	männlich	
2	09-SW-26	Schaf	CoF	männlich	
3	09-SW-37-Z	Schaf	CoF	männlich	
4	09FS7	Schaf	CoF	männlich	

Animal ID* 029019
Sire ID 829048
Dam ID 32960
Species* Schaf
Breed* Rhoe
Birthday 28-11-2000
Birthyear
Sex* männlich
Organization* Arche-Rhönschat
Latitude 51.367679
Longitude 10.732859
Photo
Comments
File /net/fs-v1/home1/zgr/henning/NHS_Kryoprc

Figure 7.31: Adding another file to an animal

7.6 Sample management

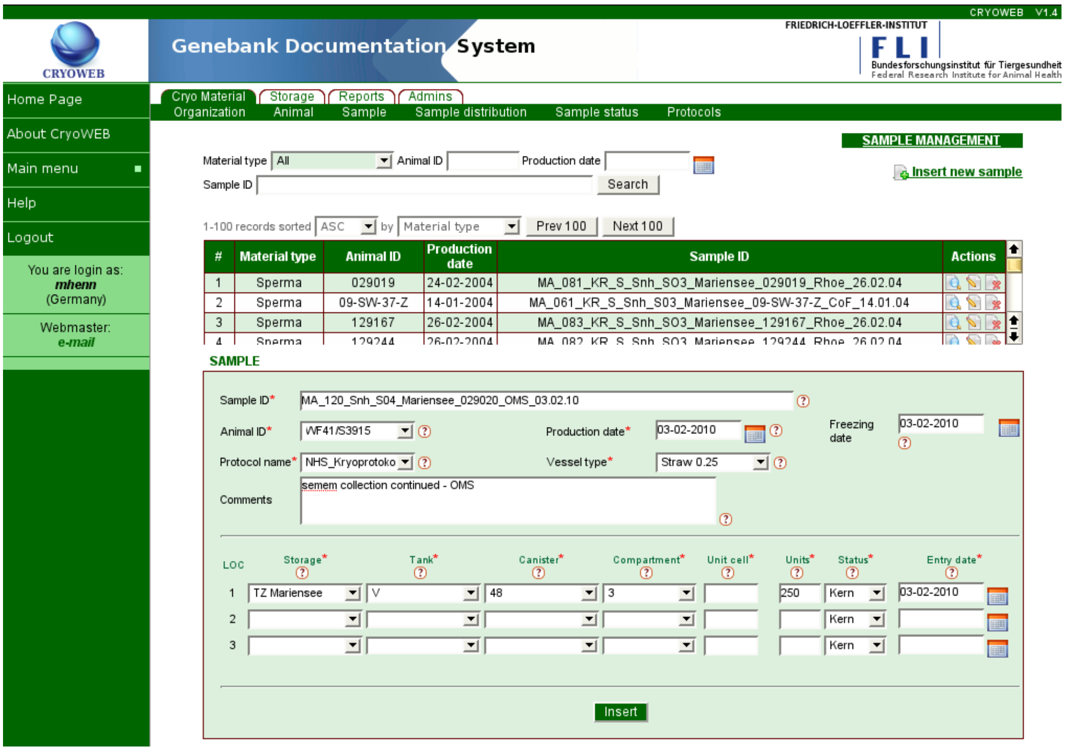
A sample is defined as the (cryo) material which is taken from an animal at a certain date. In this chapter you will learn how to enter a new sample in the database, record the sample distribution, register the sample movements and usage.

7.6.1 Adding a new sample

Open **Main Menu** ▷ **Cryo Material** ▷ **Sample**. Click the **Insert new sample** link on the right side of the page underneath the headline **Sample Management**. The **Submit** button of the form is renamed to **Insert**.

Enter the sample ID in the respective field on the data entry form. The sample ID is one of the fields which requires a special policy. So, at this stage, you should have a local policy in place. Go to the respective document and follow its rules.

Choose the donor from the **Animal ID** drop-down list. Fill in the production date of the sample by clicking the calendar and picking the right date. Choose the freezing protocol from the **Protocol name** list and the **Vessel type** from the respective list. Add any further information in addition to the freezing protocol in the **Comments** field. You may also fill the freezing date, which should be no earlier than the production date.



Material type: All
Animal ID:
Production date:
Sample ID:

1-100 records sorted ASC by Material type

#	Material type	Animal ID	Production date	Sample ID	Actions
1	Sperma	029019	24-02-2004	MA_081_KR_S_Snh_SO3_Mariensee_029019_Rhoe_26.02.04	
2	Sperma	09-SW-37-Z	14-01-2004	MA_061_KR_S_Snh_S03_Mariensee_09-SW-37-Z_CoF_14.01.04	
3	Sperma	129167	26-02-2004	MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04	
4	Sperma	129244	26-02-2004	MA_082_KR_S_Snh_SO3_Mariensee_129244_Rhoe_26.02.04	

SAMPLE

Sample ID*: MA_120_Snh_S04_Mariensee_029020_OMS_03.02.10
Animal ID*: WF41/S3915
Production date*: 03-02-2010
Freezing date: 03-02-2010
Protocol name*: NHS_Kryoprotoko
Vessel type*: Straw 0.25
Comments: semem collection continued - OMS

LOC	Storage*	Tank*	Canister*	Compartment*	Unit cell*	Units*	Status*	Entry date*
1	TZ Mariensee	V	48	3		250	Kern	03-02-2010
2							Kern	
3							Kern	

Figure 7.32: Insert new sample

In the bottom part of the form you may enter data for up to three different locations for the sample. You have to fill data for at least one location. If the sample is distributed on more than 3 locations, see chapter 7.6.2.

Choose storage location from the **Storage** drop-down list in the line for **LOC 1**. Wait until the **Tank** drop-down list got populated (the list will show '**...**') and then select the tank. Proceed to canister and compartment, in each case wait for the list to be populated with data. After selecting the storage, tank, canister and compartment, type the cell identification (last location hierarchy level) into the field **Unit cell**.

Enter the number of units (vessels) in the **Units** field and select from the **Status** drop-down list the status of the sample. The last field in line 1 to be filled is **Entry date** (the date when the sample entered the storage facilities). Fill in this field using the calendar control next to it (Figure 7.32).

For security reasons, samples are usually stored in at least 2 different locations. To add a second one, move to line 2 (LOC 2) and repeat the procedure described above. To insert data for the new sample click the **Insert** button. A confirmation dialog

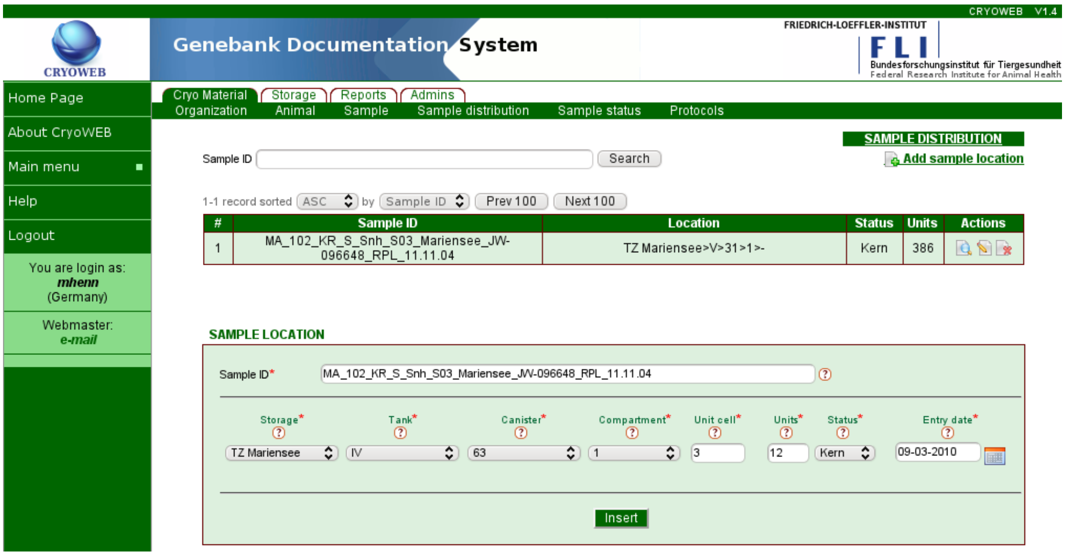
```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

7.6.2 Dealing with samples stored in more than 3 locations

If you have a new sample, distributed in more than 3 locations, you must at first insert the sample via **Sample** form, following the instructions in chapter 7.6.1, and then add data for the rest of the sample's locations via the **Sample distribution** tab. How to add a location for already recorded sample is described below.

Open **Main Menu**▷**Cryo Material**▷**Sample distribution**. Click on the **Add sample location** to start entering data. The submit button on the **Sample Location** form will be renamed to **Insert**. Fill in the **Sample ID** in the respective field in the data entry part (on the green background).



#	Sample ID	Location	Status	Units	Actions
1	MA_102_KR_S_Snh_S03_Mariensee_JW-096648_RPL_11.11.04	TZ Mariensee>V>31>1>-	Kern	386	

Sample ID*: MA_102_KR_S_Snh_S03_Mariensee_JW-096648_RPL_11.11.04

Storage*	Tank*	Canister*	Compartment*	Unit cell*	Units*	Status*	Entry date*
TZ Mariensee	IV	63	1	3	12	Kern	09-03-2010

Figure 7.33: Adding a location for sample

Select the storage location from the **Storage** drop-down list. Wait for the **Tank** list to get populated (to show '...') and choose the tank. Continue in the same manner with the **Canister** and **Compartment** lists. Type the cell identification in the **Unit cell** field.

Fill in the number of units in the **Units** field, choose legal status from the **Status** drop-down list and pick entry date from the calendar (Figure 7.33). To insert the data for the new location click **Insert**. A confirmation dialog

```
Are you sure that you want to execute this action?
```

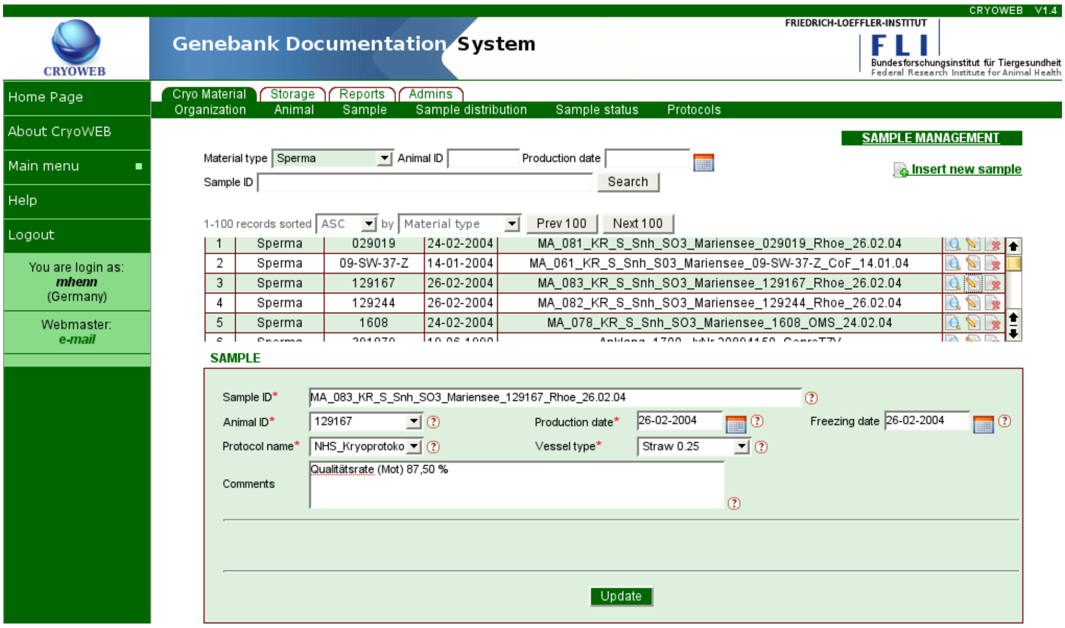
will be shown. Confirm with **OK**!

7.6.3 Correcting sample data

There are two types of corrections that can be done in the samples data. The first type are corrections in general sample data: sample id, donor animal, production date, freezing date, used protocol, type of storage vessel, comments. These are corrected via **Sample** form.

The second type of corrections deal with the sample distribution: the location of the sample, number of units, status and entry date in this location. These changes are done via **Sample distribution**.

For changes in the general sample data, open **Main Menu** ▷ **Cryo Material** ▷ **Sample**.



You are login as: ***mhenn*** (Germany)

Webmaster: *e-mail*

Material type: Sperma Animal ID: Production date:

Sample ID:

1-100 records sorted ASC by Material type

1	Sperma	029019	24-02-2004	MA_081_KR_S_Snh_SO3_Mariensee_029019_Rhoe_26.02.04
2	Sperma	09-SW-37-Z	14-01-2004	MA_061_KR_S_Snh_S03_Mariensee_09-SW-37-Z_CoF_14.01.04
3	Sperma	129167	26-02-2004	MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04
4	Sperma	129244	26-02-2004	MA_082_KR_S_Snh_SO3_Mariensee_129244_Rhoe_26.02.04
5	Sperma	1608	24-02-2004	MA_078_KR_S_Snh_SO3_Mariensee_1608_OMS_24.02.04

SAMPLE

Sample ID*: MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04

Animal ID*: 129167

Production date*: 26-02-2004

Freezing date: 26-02-2004

Protocol name*: NHS_Kryoprotoko

Vessel type*: Straw 0.25

Comments: Qualitätsrate (Mot) 87,50 %

Figure 7.34: Correct sample data

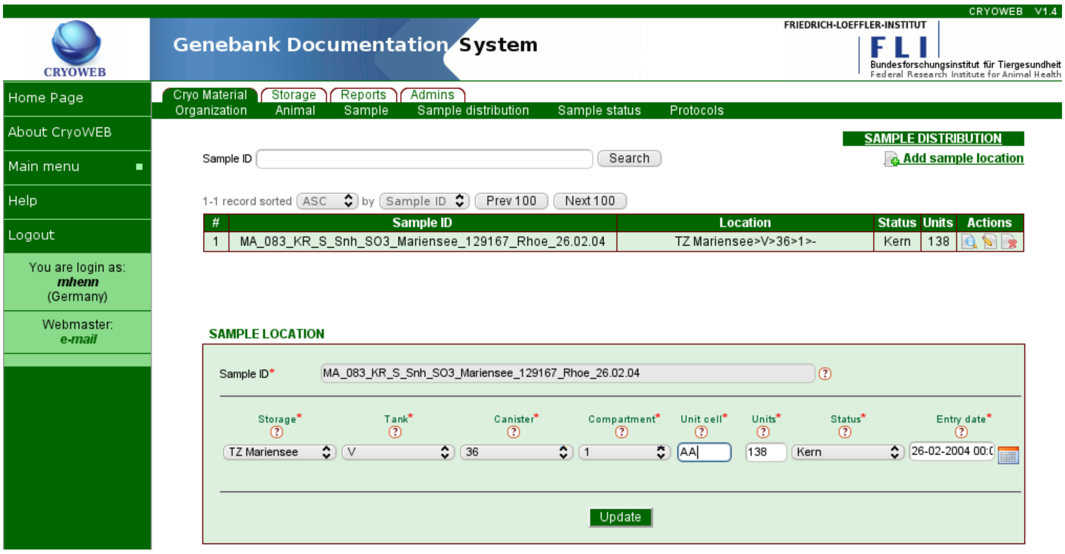
Type the sample ID in the respective field in the search part of the page. Click the **Search** button. In the results list, find the line containing the sample in question and click the **Update** (middle) icon in the **Actions** section of this line. The submit button label will change to **Update,** and the general data about the sample will be shown in the **Sample** form in the lower part of the page (Figure 7.34). Change the values you want to correct and click the **Update** button.

A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

For changes in the sample distribution part, open **Main Menu** ▷ **Cryo Material** ▷ **Sample distribution**.



#	Sample ID	Location	Status	Units	Actions
1	MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04	TZ Mariensee>V>36>1>-	Kern	138	

Sample ID* MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04

Storage*	Tank*	Canister*	Compartment*	Unit cell*	Units*	Status*	Entry date*
TZ Mariensee	V	36	1	AA	138	Kern	26-02-2004 00:(

Figure 7.35: Correct sample location data

Enter the sample identification in the **Sample ID** field in the search part of the form. Click the **Search** button. In the results list, find the line containing the sample in question and click the **Update** (middle) icon in the **Actions** section of this line. Correct the wrong data (e.g. location of the sample, number of units, status, entry date). Click the **Update** button to submit the changes (Figure 7.35). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

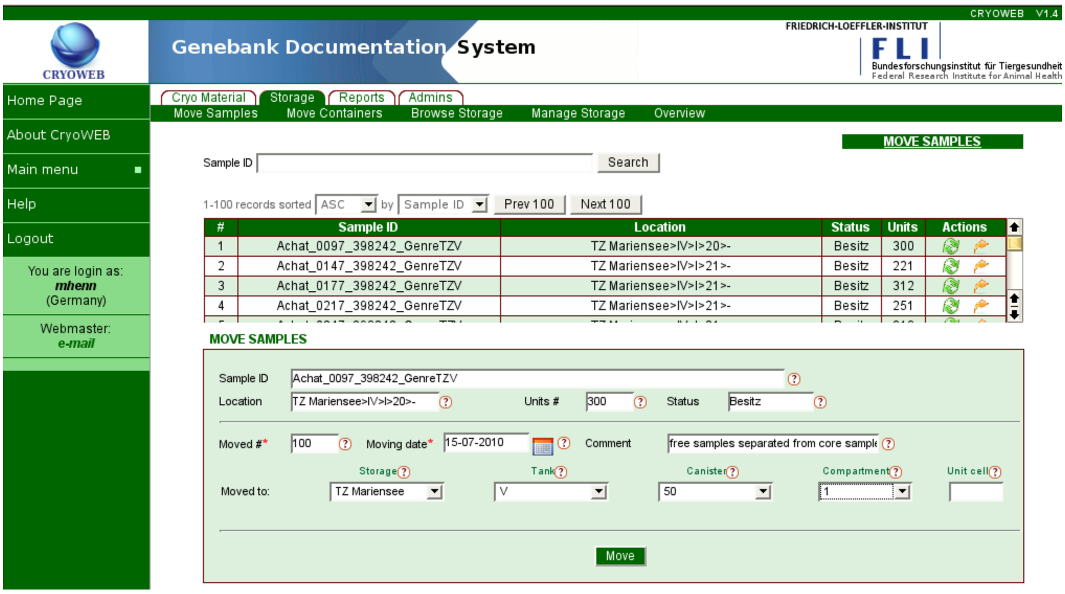
> **Note:** If you try to change the production or freezing date to a value that is in conflict with the existing data in the database, the system will reject the changes. For example, if you 'correct' the production date to be after the entry date, you will get an error message.

7.6.4 Moving sample units into another location

Each physical movement of samples has to be registered in the database. There are two types of sample movements. Samples can be moved from one location to another within the genebank, e.g. from one tank to another. On the other hand the samples can be used, or sold to various organizations. We say that the samples are "moved", if the target destination is somewhere within the genebank, and "removed" if samples are used or taken to storage, which does not belong to the genebank. If you want to record the fact that part of a sample has been used, go to 7.6.5.

Open **Main Menu** ▷ **Storage** ▷ **Move Samples**. Enter a sample ID in the search part of the form and click the **Search** button. If the sample is recorded in the database, the results list will contain records for the present location as well as status and number of units in each location.

To move part of the sample to another location in the genebank, click the **Move** icon (left one) in the line containing the source location from where the units will be moved. The label of the submit button on the form will change to **Move**.



#	Sample ID	Location	Status	Units	Actions
1	Achat_0097_398242_GenreTZV	TZ Mariensee>IV>I>20>-	Besitz	300	
2	Achat_0147_398242_GenreTZV	TZ Mariensee>IV>I>21>-	Besitz	221	
3	Achat_0177_398242_GenreTZV	TZ Mariensee>IV>I>21>-	Besitz	312	
4	Achat_0217_398242_GenreTZV	TZ Mariensee>IV>I>21>-	Besitz	251	

MOVE SAMPLES

Sample ID: Achat_0097_398242_GenreTZV

Location: TZ Mariensee>IV>I>20>- Units #: 300 Status: Besitz

Moved #*: 100 Moving date*: 15-07-2010 Comment: free samples separated from core sampl

Moved to: Storage: TZ Mariensee Tank: V Canister: 50 Compartment: 1 Unit cell:

Figure 7.36: Move sample units into another location

In the form **Move Samples** the sample number, the source location, the number of units and the status are filled by the system. Fill in the number of units to be moved into the field **Moved** #, pick date of movement using the calendar, and write comments (e.g reasons for movement of the samples) in the comment field.

Choose the target location by selecting first the **Storage**, then **Tank**, **Canister**, **Compartment** and filling the unit cell. Always wait, after selecting a value from the drop-down list, for the next one to be populated. Click the **Move** button (Figure 7.36). A confirmation dialog

```
    Are you sure that you want to execute this action?
```

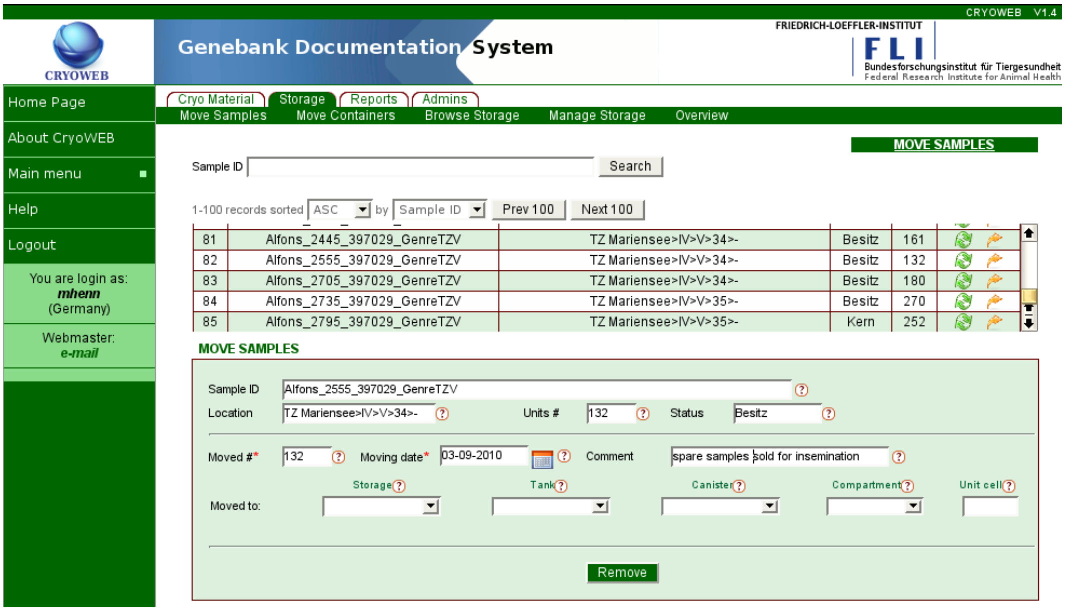
will be shown. Confirm with **OK**!

7.6.5 Using (removing) samples

Open **Main Menu** ▷ **Storage** ▷ **Move Samples**. Enter a sample ID in the search part of the form and click the **Search** button. If the sample is recorded in the database, the results list will contain records for the present location as well as status and number of units in each location.

To remove part of the sample from the genebank (e.g. if it is to be used), click the **Remove** icon (left one) in the line containing the source location from where the units were removed. The label of the submit button on the form will change to **Remove**.

In the form **Move Samples** the sample number, the source location, the number of units and the status are filled by the system. Fill in the number of units to be removed into the field **Moved #**, pick date of movement using the calendar, and write comments (e.g reasons for the removal) in the comment field.



81	Alfons_2445_397029_GenreTZV	TZ Mariensee>IV>V>34>-	Besitz	161
82	Alfons_2555_397029_GenreTZV	TZ Mariensee>IV>V>34>-	Besitz	132
83	Alfons_2705_397029_GenreTZV	TZ Mariensee>IV>V>34>-	Besitz	180
84	Alfons_2735_397029_GenreTZV	TZ Mariensee>IV>V>35>-	Besitz	270
85	Alfons_2795_397029_GenreTZV	TZ Mariensee>IV>V>35>-	Kern	252

Sample ID: Alfons_2555_397029_GenreTZV
Location: TZ Mariensee>IV>V>34>-
Units #: 132
Status: Besitz
Moved #*: 132
Moving date*: 03-09-2010
Comment: spare samples sold for insemination

Figure 7.37: Remove sample from the genebank

Do not select anything from the drop-down lines in the **Moved to:** line. Instead, click the **Remove** button (Figure 7.37). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

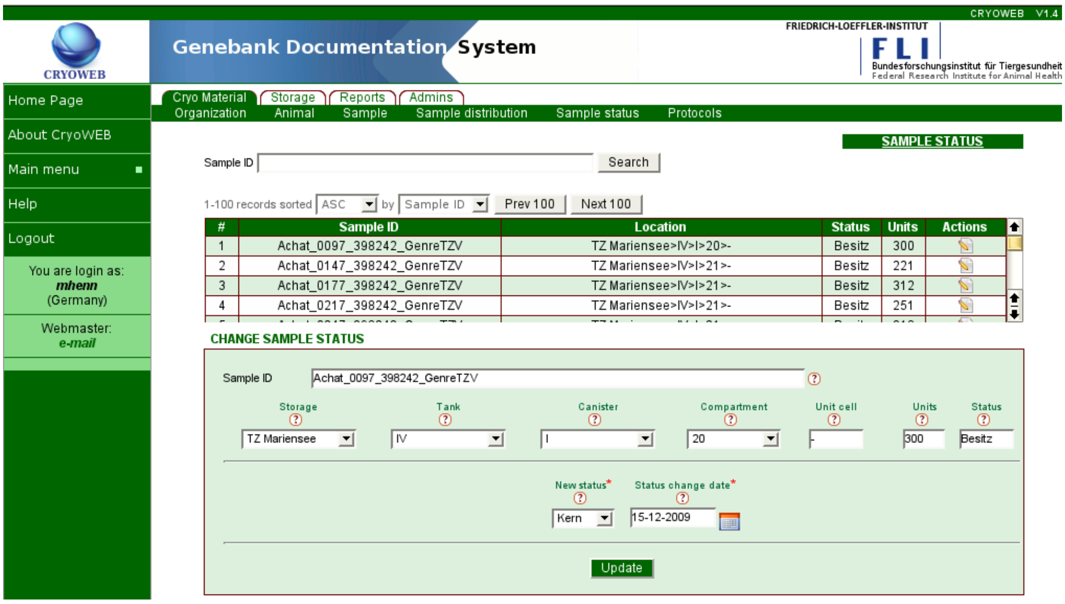
> **Note:** You can remove only samples, which do not have ’core’ status, as CryoWEB has an inbuilt protection to prevent the direct removal of core samples. This is done to safeguard against unintended removals of core material. If you want to remove or use part of a core sample, move this part to another (virtual) location in the genebank and there change its status to free. Then, you can remove the free units from the genebank.

7.6.6 Changing the status of sample units

For the **Status** of a sample, three classes are fixed. In most countries a scientific committee decides on a list of endangered breeds and the amount and type of material to be stored in the genebank. In each country there must be a policy for the time period, during which a core set of cryo material from a given breed should be kept intact.

If more cryo material from a breed is available in the genebank and does not belong to the core set, it may be used for breeding purposes with the owners agreement (owned).

For the third class of material which might be part of the National genebank, the access may be free. Generally speaking, it is up to the genebank manager to define sample status and its meaning. However, the status ’core’ is treated differently, as described above.



#	Sample ID	Location	Status	Units	Actions
1	Achat_0097_398242_GenreTZV	TZ Mariensee>IV>I>20>-	Besitz	300	
2	Achat_0147_398242_GenreTZV	TZ Mariensee>IV>I>21>-	Besitz	221	
3	Achat_0177_398242_GenreTZV	TZ Mariensee>IV>I>21>-	Besitz	312	
4	Achat_0217_398242_GenreTZV	TZ Mariensee>IV>I>21>-	Besitz	251	

Sample ID: Achat_0097_398242_GenreTZV

Storage	Tank	Canister	Compartment	Unit cell	Units	Status
TZ Mariensee	IV	I	20	-	300	Besitz

New status*: Kern
Status change date*: 15-12-2009

Figure 7.38: Change the status of sample units

Open **Main Menu** ▷ **Cryo Material** ▷ **Sample status**. Enter the **Sample ID** in the search part of the form and click the **Search** button. If the sample is present in the genebank, its current distribution within the storage will be listed in the results table. Only one action may be executed - the icon with the pencil allows updating of sample status. Click the icon and all the information available for this part of the sample will be shown in the form below (first two lines).

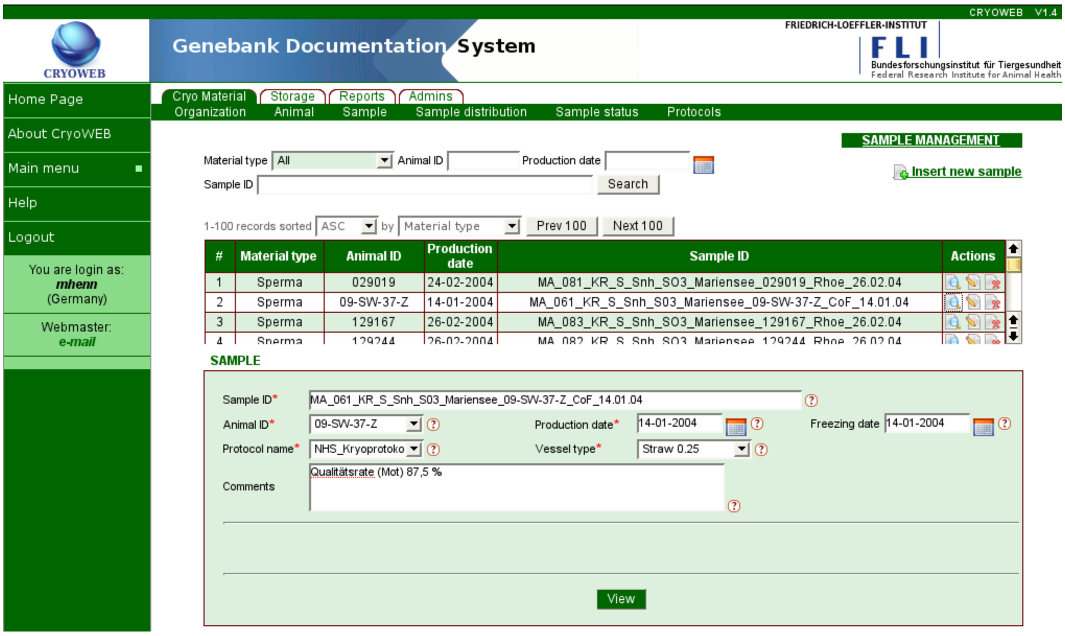
Choose the new status from the list **New status**, enter the date of change by picking it from the calendar control, then click the **Update** button to submit data to the database (Figure 7.38). A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**!

7.6.7 Searching samples in the database

Open **Main Menu** ▷ **Cryo Material** ▷ **Sample**. First you have to choose from the **Material type** list, what type of samples you are searching for (Figure 7.39). In case you do not know the material, type choose **All**. You can fill in one or more from the other 3 search fields - **Animal ID**, **Production date** and **Sample ID** and the search will be filtered by all these criteria. To start the search click on the **Search** button. Depending on the data stored in your database the search may take some time, in which a progress bar is shown on the screen. When the results are shown, you can sort them by **Material type**, **Animal ID**, **Production date** and/or **Sample ID** in ascending or descending order.



Material type: All
Animal ID:
Production date:
Sample ID:

1-100 records sorted ASC by Material type

#	Material type	Animal ID	Production date	Sample ID	Actions
1	Sperma	029019	24-02-2004	MA_081_KR_S_Snh_SO3_Mariensee_029019_Rhoe_26.02.04	
2	Sperma	09-SW-37-Z	14-01-2004	MA_061_KR_S_Snh_S03_Mariensee_09-SW-37-Z_CoF_14.01.04	
3	Sperma	129167	26-02-2004	MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04	
4	Sperma	129244	26-02-2004	MA_082_KR_S_Snh_SO3_Mariensee_129244_Rhoe_26.02.04	

SAMPLE

Sample ID*: MA_061_KR_S_Snh_S03_Mariensee_09-SW-37-Z_CoF_14.01.04
Animal ID*: 09-SW-37-Z
Production date*: 14-01-2004
Freezing date: 14-01-2004
Protocol name*: NHS_Kryoprotoko
Vessel type*: Straw 0.25
Comments: Qualitätsrate (Mot) 87,5 %

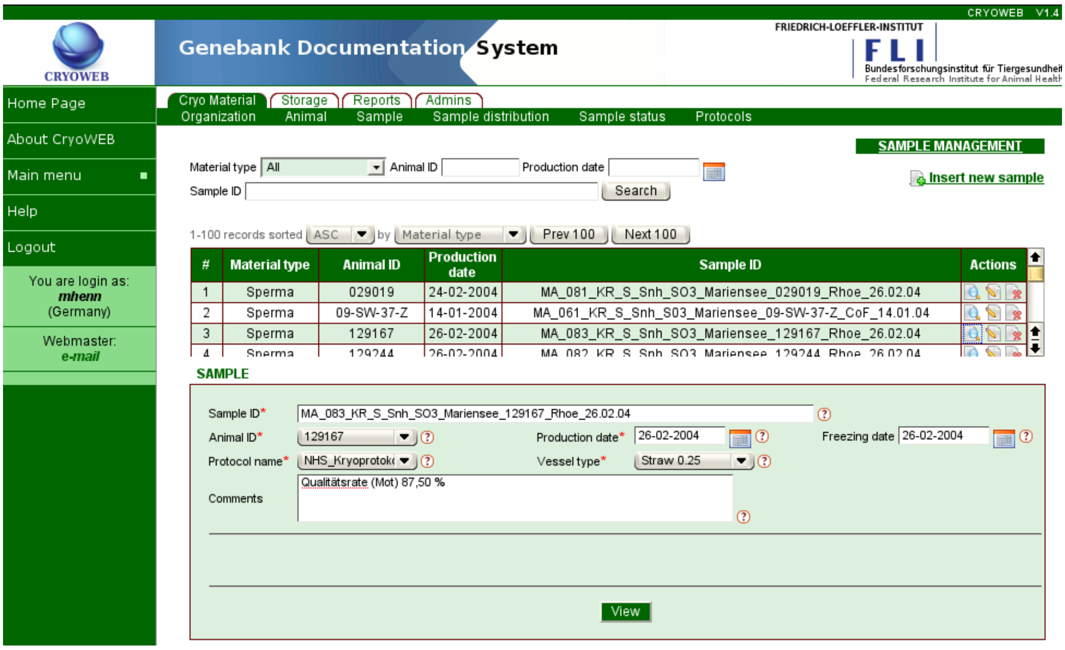
Figure 7.39: Search all samples in the database

Several examples:

- To find all blood samples, choose **Blood** from the **Material type** list and click on the **Search** button.
- To find all samples from a single animal, fill the **Animal ID** search field and click on the **Search** button.
- To find all blood samples from a single animal, choose **Blood** from the **Material type** list, fill the **Animal ID** field and click on the **Search** button.
- To find all blood samples produced on a certain date, choose **Blood** from the **Material type** list, fill the **Production date** field and click on the **Search** button.
- To find all samples with identifications starting with **DE102** type DE102 in the **Sample ID** search field, choose **All** from the **Material type** list and click on the **Search** button.

7.6.8 Viewing general sample data

Open **Main Menu** ▷ **Cryo material** ▷ **Sample**. Then search for the sample as described in 7.6.7.



Material type All Animal ID Production date

Sample ID

1-100 records sorted ASC by Material type

#	Material type	Animal ID	Production date	Sample ID	Actions
1	Sperma	029019	24-02-2004	MA_081_KR_S_Snh_SO3_Mariensee_029019_Rhoe_26.02.04	
2	Sperma	09-SW-37-Z	14-01-2004	MA_061_KR_S_Snh_S03_Mariensee_09-SW-37-Z_CoF_14.01.04	
3	Sperma	129167	26-02-2004	MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04	
4	Sperma	129244	26-02-2004	MA_082_KR_S_Snh_SO3_Mariensee_129244_Rhoe_26.02.04	

Sample ID* MA_083_KR_S_Snh_SO3_Mariensee_129167_Rhoe_26.02.04

Animal ID* 129167 Production date* 26-02-2004 Freezing date 26-02-2004

Protocol name* NHS_Kryoprotok Vessel type* Straw 0.25

Comments Qualitätsrate (Mot) 87,50 %

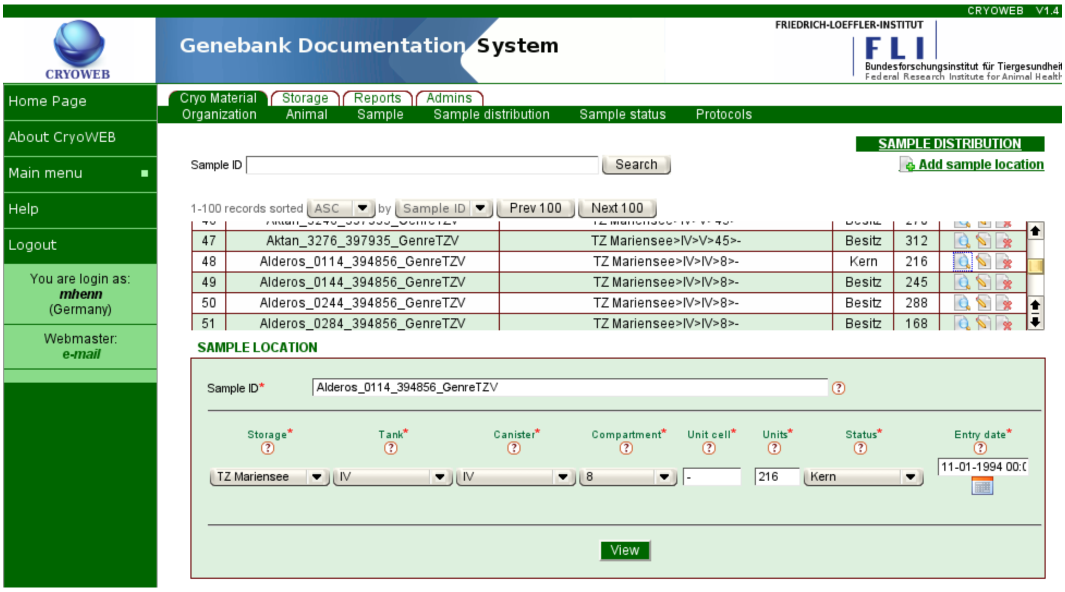
Figure 7.40: View general sample data

Summaries of all sample records are shown in the search result table in groups of 100. These summaries include the material type, animal ID, production date and the

ID of the sample. To view the complete data for a certain sample, navigate through the table of samples (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the **Sample ID** you are looking for. Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The general sample data will be shown in the **Sample** form below (Figure 7.40).

7.6.9 Viewing sample distribution data

Open **Main Menu** ▷ **Cryo material** ▷ **Sample distribution**.



47	Aktan_3276_397935_GenreTZV	TZ Mariensee>IV>V>45>-	Besitz	312
48	Alderos_0114_394856_GenreTZV	TZ Mariensee>IV>IV>8>-	Kern	216
49	Alderos_0144_394856_GenreTZV	TZ Mariensee>IV>IV>8>-	Besitz	245
50	Alderos_0244_394856_GenreTZV	TZ Mariensee>IV>IV>8>-	Besitz	288
51	Alderos_0284_394856_GenreTZV	TZ Mariensee>IV>IV>8>-	Besitz	168

Sample ID*: Alderos_0114_394856_GenreTZV

Storage*	Tank*	Canister*	Compartment*	Unit cell*	Units*	Status*	Entry date*
TZ Mariensee	IV	IV	8	-	216	Kern	11-01-1994 00:

Figure 7.41: View sample's distribution data

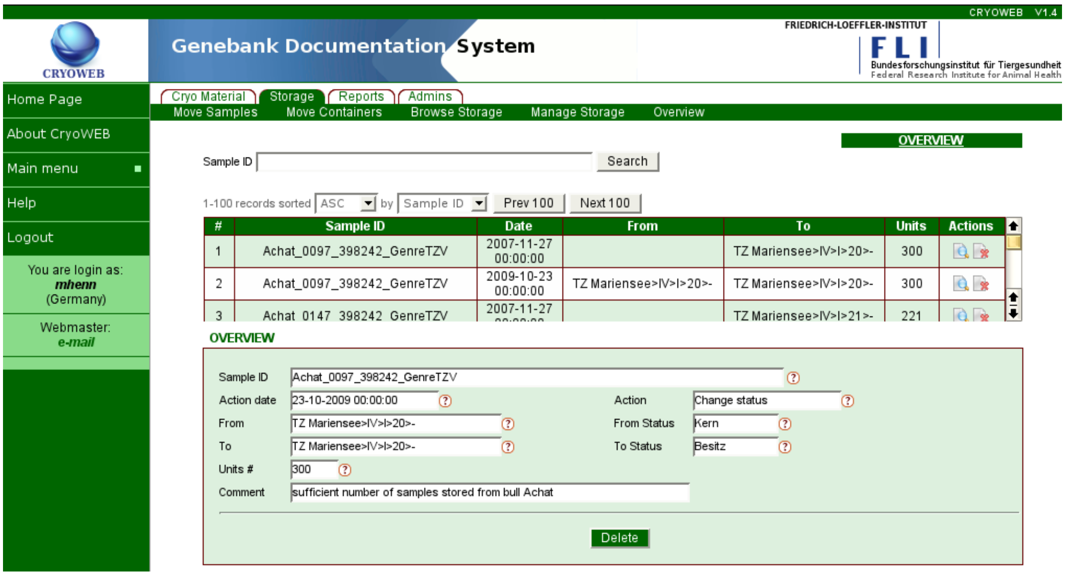
Summaries of all sample distribution records are shown in the search result table in groups of 100. These summaries include the sample ID, the location, the number of sample's units stored there and their status. To view the complete data for a certain sample location, navigate through the table of samples distribution (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the **Sample ID** and the **Location** you are looking for. Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for this distribution record will be shown in the **Sample location** form below (Figure 7.41).

7.6.10 Reverting movement or status change

You can only update the last action - movement or change of status, but not the second last. So you have to delete the last action and then update second last one. Open **Main Menu** ▷ **Storage** ▷ **Overview**, fill the sample identification in the **Sample ID** search field and click the **Search** button. If such sample is present in the genebank, all the movements/status changes of units from this sample will be listed in the results table in chronological order. Find the last line in the list and click the **Delete** (right) icon in the Actions section of this line (Figure 7.42). The data for the chosen action will be filled in the **Overview** form and the submit button will change its label to **Delete**. To revert the action click on the **Delete** button. A confirmation dialog

```
Are you sure that you want to execute this action?
```

will be shown. Confirm with **OK**! The action is reverted, i.e. in case of movement the units are returned to the previous location, and the last movement record is erased. Once reverted, the action cannot be automatically restored.



#	Sample ID	Date	From	To	Units	Actions
1	Achat_0097_398242_GenreTZV	2007-11-27 00:00:00		TZ Mariensee>IV>I>20>-	300	
2	Achat_0097_398242_GenreTZV	2009-10-23 00:00:00	TZ Mariensee>IV>I>20>-	TZ Mariensee>IV>I>20>-	300	
3	Achat 0147 398242 GenreTZV	2007-11-27		TZ Mariensee>IV>I>21>-	221	

Sample ID: Achat_0097_398242_GenreTZV
Action date: 23-10-2009 00:00:00
Action: Change status
From: TZ Mariensee>IV>I>20>-
From Status: Kern
To: TZ Mariensee>IV>I>20>-
To Status: Besitz
Units #: 300
Comment: sufficient number of samples stored from bull Achat

Figure 7.42: Revert status change

7.7 Reports

In this section you will find a short description of each report, which can be generated by CryoWEB in PDF format, along with the options for exporting data to other applications.

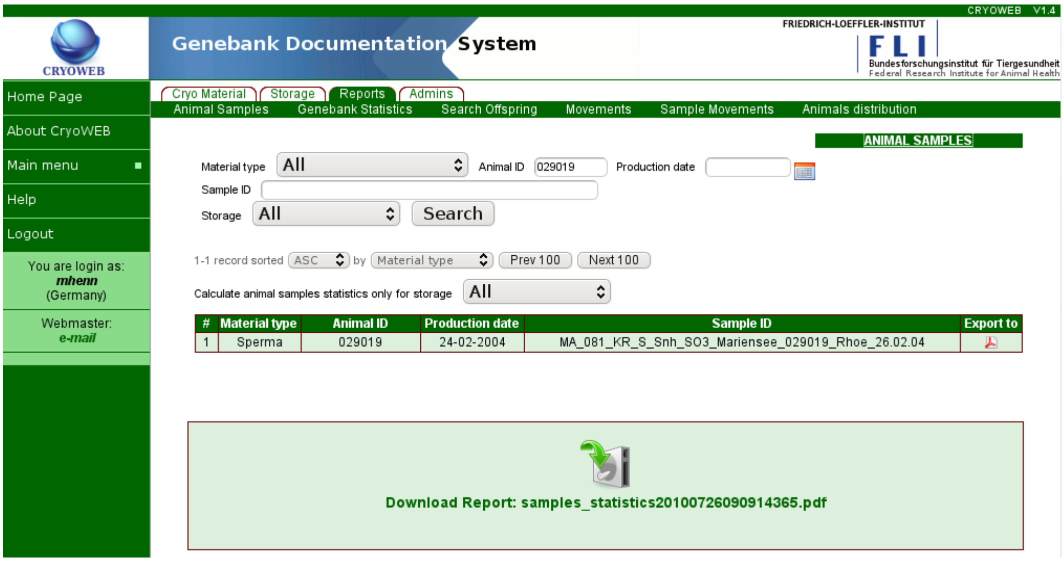
7.7.1 List all samples of an animal

This report has two parts - a summary of the animal's characteristics in the heading of the report, and a list of the samples produced from that animal and their distribution.

Each line of this list represents a group of units from a sample, which are stored in one location and have the same legal status.

Open **Cryo Material** ▷ **Reports** ▷ **Animal Samples**. Choose material type from the respective drop-down list in the search part, fill in the **Animal ID** field and click the **Search** button. A list of results will be shown including **Material type**, **Animal ID**, **Production date** and **Sample ID**. Click the **PDF** icon in the column **Export to** to generate the report in PDF format. To download/open the report, click on the link **Download Report:...** (Figure 7.43).

The report can be generated also for a certain location. In this case, prior to creating the report via the **PDF** icon, you should choose a storage place from the list near "Calculate animal samples statistics only for storage".



You are login as: mhenn (Germany)

Material type: All

Animal ID: 029019

Production date:

Sample ID:

Storage: All

1-1 record sorted ASC by Material type

Calculate animal samples statistics only for storage: All

#	Material type	Animal ID	Production date	Sample ID	Export to
1	Sperma	029019	24-02-2004	MA_081_KR_S_Snh_SO3_Mariensee_029019_Rhoe_26.02.04	

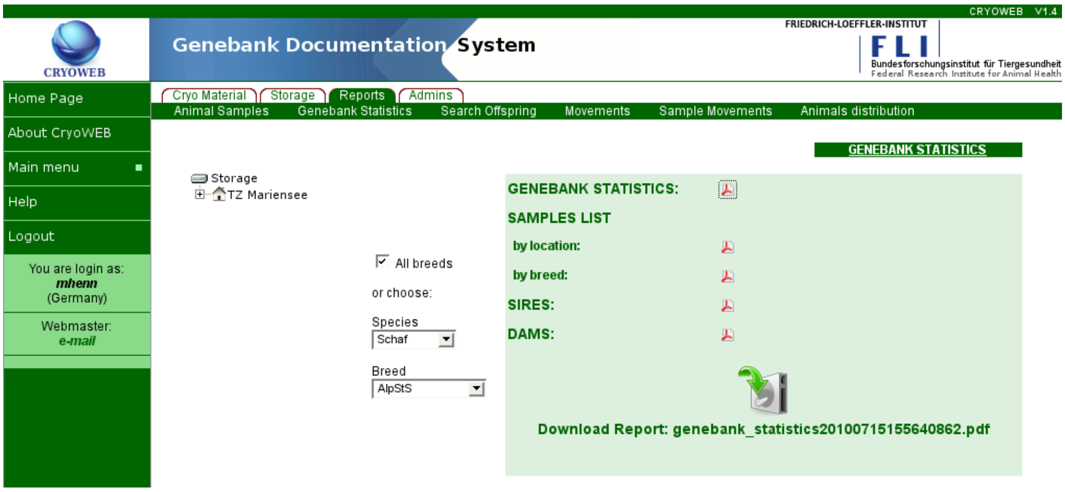
Download Report: samples_statistics20100726090914365.pdf

Figure 7.43: List all samples of an animal

7.7.2 Accumulated statistics per breed, material and location

This report lists the number of samples and units by material type and breed with aggregation of total number of samples per species. This is a general overview of all the material stored in the genebank and can be used to control the current situation in comparison to the targets of the conservation program.

Open **Main Menu** ▷ **Reports** ▷ **Genebank statistics**. Click on **Storage** if you want a report for the whole genebank, or click on a certain storage name if you want a report only for this location. Select the **All breeds** check box, if you want statistics for all breeds, or choose species and breed from the respective drop-down lists to filter the statistics for a single breed. Click the **PDF** icon on the chosen report to generate the report in PDF format, e.g. the **GENEBANK STATISTICS** as shown in Figure 7.44. To download/open the report click on the link **Download Report:...**.



You are login as: mhenn (Germany)

☑ All breeds

or choose:

Species: Schaf

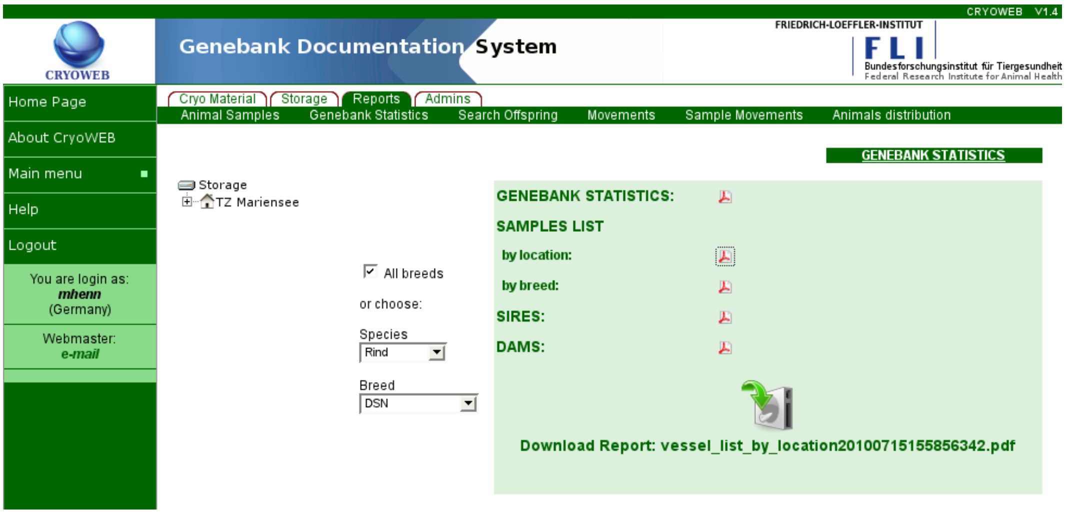
Breed: AlpStS

Download Report: genebank_statistics20100715155640862.pdf

Figure 7.44: Accumulated statistics per breed, material and location

7.7.3 List all samples in location

This report lists all the samples stored in one location, grouped by breed and species. This is an inventory list for a given storage, which can be used for checks.



You are login as: mhenn (Germany)

☑ All breeds

or choose:

Species: Rind

Breed: DSN

Download Report: vessel_list_by_location20100715155856342.pdf

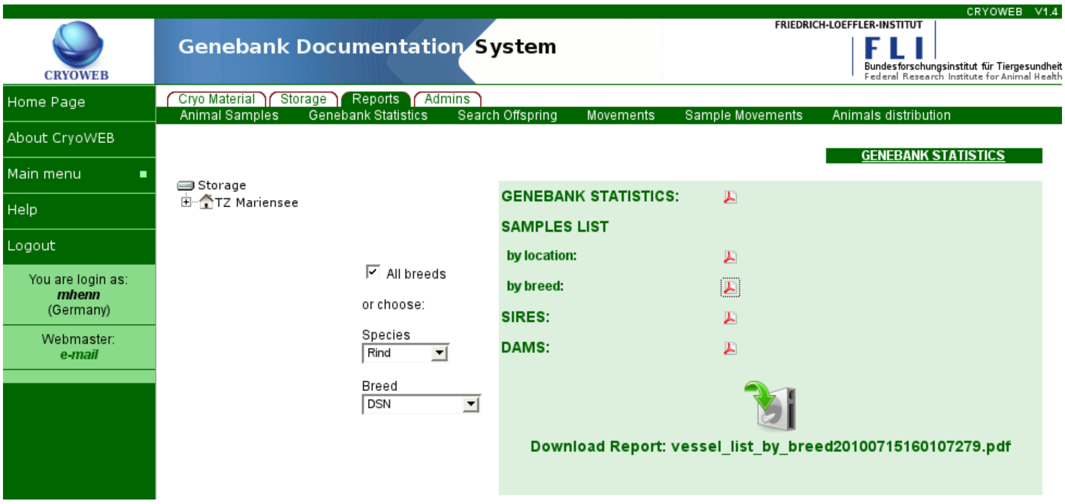
Figure 7.45: List all samples in location

Open **Main Menu** ▷ **Reports** ▷ **Genebank statistics**. Click on **Storage** if you want a report for the whole genebank, or click on a certain storage name if you want report only for this location. Select the **All breeds** check box, if you want statistics for all breeds or choose species and breed from the respective drop-down lists to filter the statistics for a single breed. Click the **PDF** icon on the **SAMPLES LIST by location** line to generate the report in PDF format. To download/open the report click on the link **Download Report:...** (Figure 7.45).

7.7.4 List all samples from a breed

This report lists all the samples for one breed, produced by animals from this breed, grouped by location. This document can be used by a breed society to control the amount of stored material and its location in management of a conservation program.

Open **Main Menu** ▷ **Reports** ▷ **Genebank statistics**. Click on **Storage** if you want a report for the whole genebank, or click on a certain storage name, if you want report only for this location. Select the **All breeds** check box, if you want statistics for all breeds, or choose species and breed from the respective drop-down lists to filter the statistics for a single breed. Click the **PDF** icon on the **SAMPLES LIST by breed** line to generate the report in PDF format. To download/open the report click on the link **Download Report:...** (Figure 7.46).



You are login as: *mhenn* (Germany)

Webmaster: *e-mail*

☑ All breeds

or choose:

Species: Rind

Breed: DSN

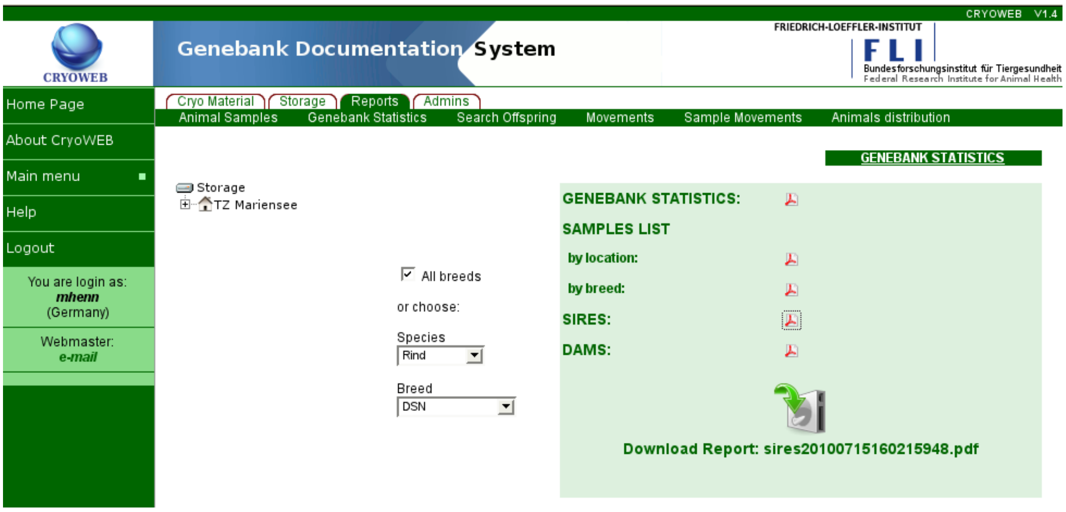
Download Report: vessel_list_by_breed20100715160107279.pdf

Figure 7.46: Sample list by breed

7.7.5 Average number of samples per material from male animals

This report lists the total number of male donors per breed and species along with the minimum, maximum and average number of sample units from male donors per material type and breed.

Open **Main Menu** ▷ **Reports** ▷ **Genebank statistics.** Click on **Storage** if you want a report for the whole genebank, or click on a certain storage name if you want report only for this location. Select the **All breeds** check box if you want statistics for all breeds or choose species and breed from the respective drop-down lists to filter the statistics for a single breed. Click the **PDF** icon on the **SIRES** line to generate the report in PDF format. To download/open the report click on the link **Download Report:...** (Figure 7.47).



You are login as: **mhenn** (Germany)

☑ All breeds

or choose:

Species: Rind

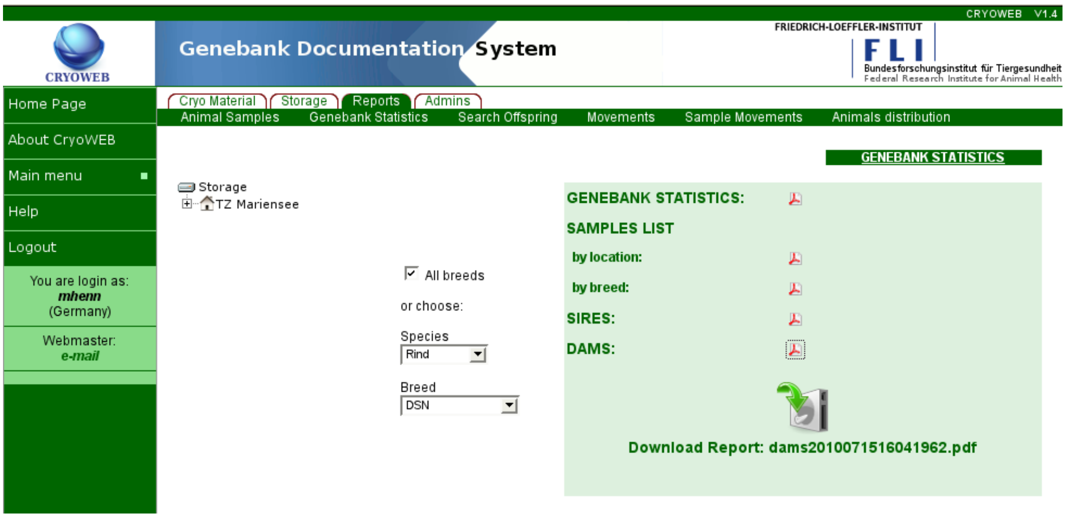
Breed: DSN

Download Report: sires20100715160215948.pdf

Figure 7.47: List of sires

7.7.6 Average number of samples per material from female animals

This report lists the total number of female donors per breed and species along with the minimum, maximum and average number of sample units from female donors per material type and breed.



You are login as: **mhenn** (Germany)

☑ All breeds

or choose:

Species: Rind

Breed: DSN

Download Report: dams2010071516041962.pdf

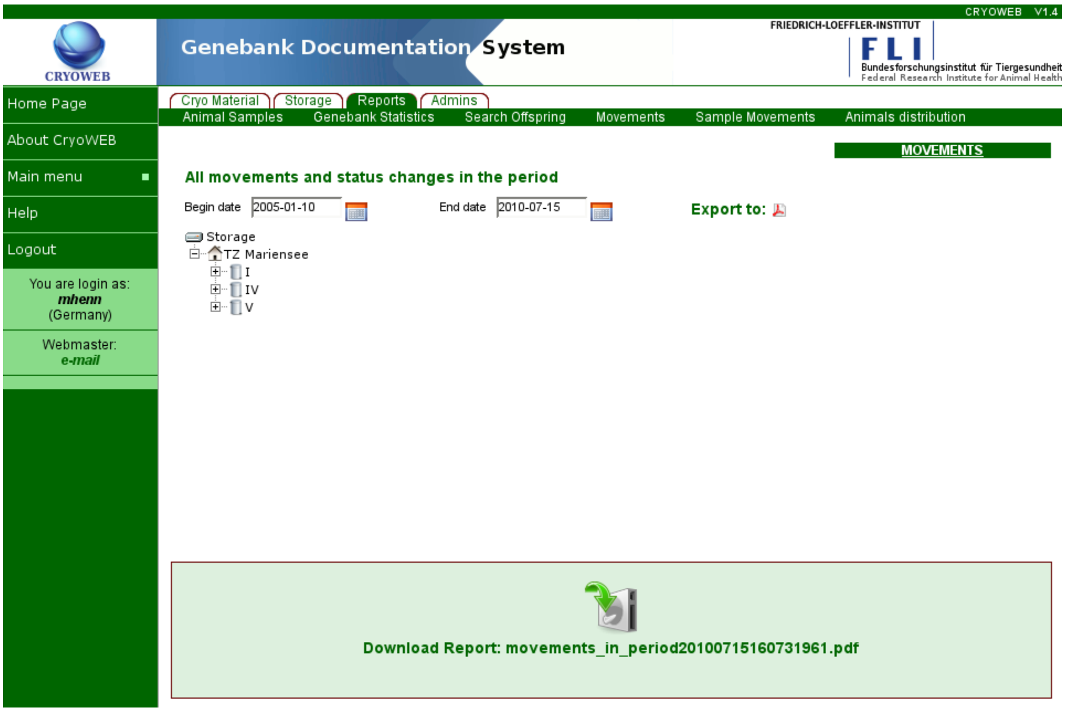
Figure 7.48: List of dams

Open **Main Menu** ▷ **Reports** ▷ **Genebank statistics.** Click on **Storage** if you want a report for the whole genebank, or click on a certain storage name if you want report only for this location. Select the **All breeds** check box if you want statistics for all breeds or choose species and breed from the respective drop-down lists to filter the statistics for a single breed. Click the **PDF** icon on the **DAMS** line to generate the report in PDF (format). To download/open the report click on the link **Download Report:...** (Figure 7.48).

7.7.7 List all material movements and status changes in a given period

This report lists all inserts of new samples, movements and status changes in the period chosen by the user. For each action the sample identification, the material type, the legal status, the number of inserted/moved units, the action date and the source (**From**) and target (**To**) locations are listed.

In case of insert the **From** location is empty. In case of status change the **From** and **To** locations are the same and the status listed is the new one. In case the sample is removed from the genebank, e.g. sold, the **To** location is empty. The report can be filtered by movements from/to a single storage place, single tank, canister, compartment, or even to single cell (goblet).



You are login as: **mhenn** (Germany)

Webmaster: *e-mail*

All movements and status changes in the period

Begin date 2005-01-10

End date 2010-07-15

Export to:

Storage
- TZ Mariensee
  - I
  - IV
  - V

Download Report: movements_in_period20100715160731961.pdf

Figure 7.49: List of all material movements between 10.01.2005 and 15.07.2010

Open **Main Menu** ▷ **Reports** ▷ **Movements**. Click on **Storage** if you want a report for the whole genebank, or click on a certain storage name if you want report only for this location (you can choose any level).

Click the **PDF** icon next to **Export to** to generate the report in PDF (format). To download/open the report click on the link **Download Report:...** (Figure 7.49).

7.7.8 List all movements of a given sample

This report is intended to list, in chronological order, all movements of the sample parts, starting with the initial insert of the sample in the storage locations. The report includes source and target locations, the number of moved units and their legal status. Also status changes are shown in the report.

To recognize what was the action shown in a certain line, you should look at the source (**From**) and target (**To**) locations.

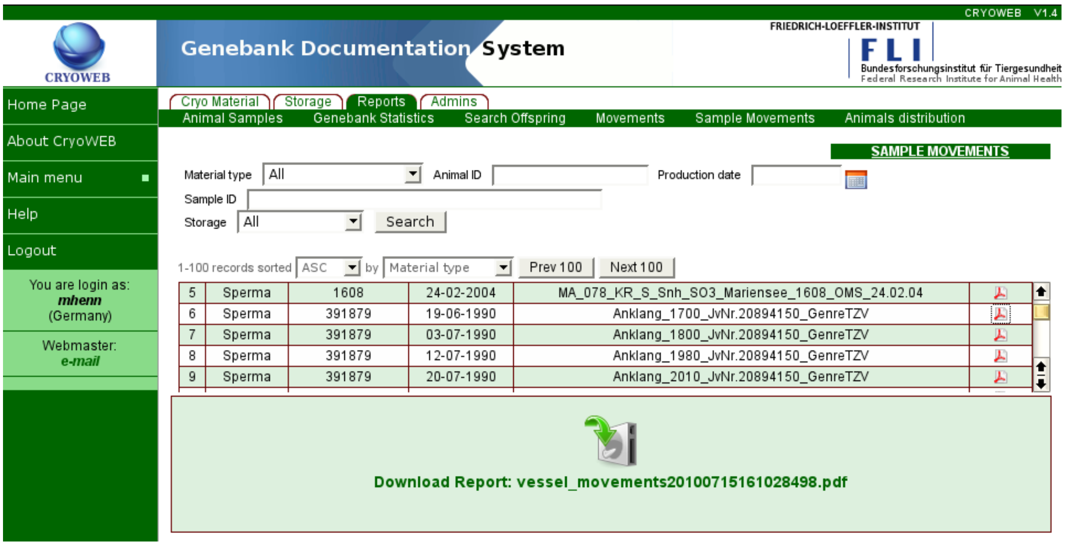
If the source location is empty, this is an insert.

If the target location is empty, then the sample was taken out of the genebank.

If the source and target locations are filled and different, this is a movement from one location to another.

And, finally, if the source and target locations are the same, this was a change in the sample's status. In such case the new status is shown in the column **Status**.

Open **Main Menu** ▷ **Reports** ▷ **Sample Movements**. Fill in the identification of the sample for which you want to generate report in the **Sample ID** field, choose for **Material type** and for **Storage All** and click the **Search** button. If such sample exists in the database it will be listed in the results table below. Click the **PDF** icon in the column **Export to** to generate report in PDF format. To download/open the report click on the link **Download Report:...** (Figure 7.50).



You are login as:
mhenn
(Germany)

Material type: All
Animal ID:
Production date:
Sample ID:
Storage: All

1-100 records sorted ASC by Material type

5	Sperma	1608	24-02-2004	MA_078_KR_S_Snh_SO3_Mariensee_1608_OMS_24.02.04	
6	Sperma	391879	19-06-1990	Anklang_1700_JvNr.20894150_GenreTZV	
7	Sperma	391879	03-07-1990	Anklang_1800_JvNr.20894150_GenreTZV	
8	Sperma	391879	12-07-1990	Anklang_1980_JvNr.20894150_GenreTZV	
9	Sperma	391879	20-07-1990	Anklang_2010_JvNr.20894150_GenreTZV	

Download Report: vessel_movements20100715161028498.pdf

Figure 7.50: List of all sample movements

7.7.9 Browsing the distribution of the animals from a given breed

In case the location of the animal donor was recorded in the database (the **Longitude** and **Latitude** fields on the **Animal** form), their distribution in the country can be visualized on a map on a per breed basis. Thereby, the geographical distribution of a breed can be visualized.

Open **Main Menu** ▷ **Reports** ▷ **Animals distribution**. Choose the species from the respective drop-down list. If the species you want to select is on the first place in the list, select the next one, and then select again the first item in the list. Wait until the breed list is populated and select the breed. Click the **Export data** link. When the file is generated click on **Show map** button. A map provided by **OpenStreetMap** will be shown and the animals are visualized by orange dots (Figure 7.51). Zoom the map to see the precise location of the animals.

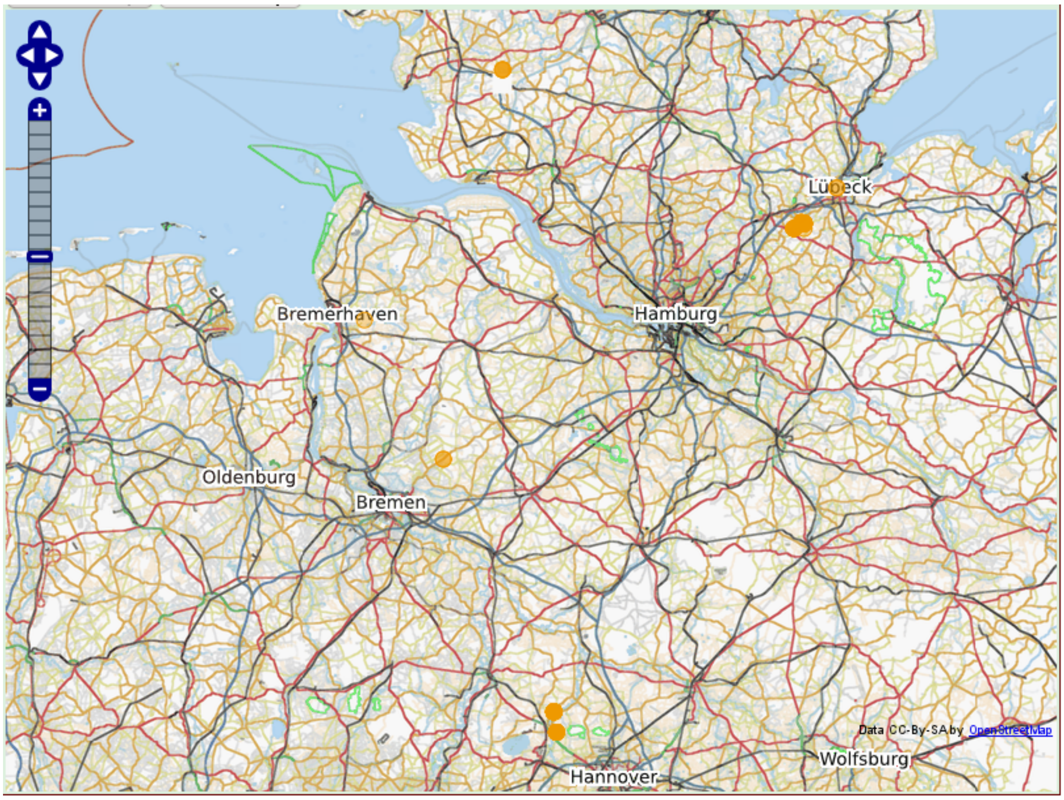


Figure 7.51: Distribution of the donors from DSN breed

7.7.10 Exporting the location of donors from given breed for Google Earth

If the location coordinates of the animal donors were recorded, their distribution per breed can be visualized over the satellite imagery, maps and terrain offered by

Google Earth. There the animal location along with the animal data and amount of stored material from that animal will be shown. As a prerequisite you must have the Google Earth software installed on your computer.

Open **Main Menu** ▷ **Reports** ▷ **Animals distribution**. Choose the species from the respective drop-down list. Wait until the breed list is populated and select the breed. Click the **Export data** link. When the file is generated, click on the **Download the file and open it in Google Earth...** to save the file on your computer. Start the **Google Earth** software and there click **File** ▷ **Open** and choose the file you have saved from CryoWEB. The animals will be shown on the map and listed in the **Places** tree as shown in Figure 7.52.

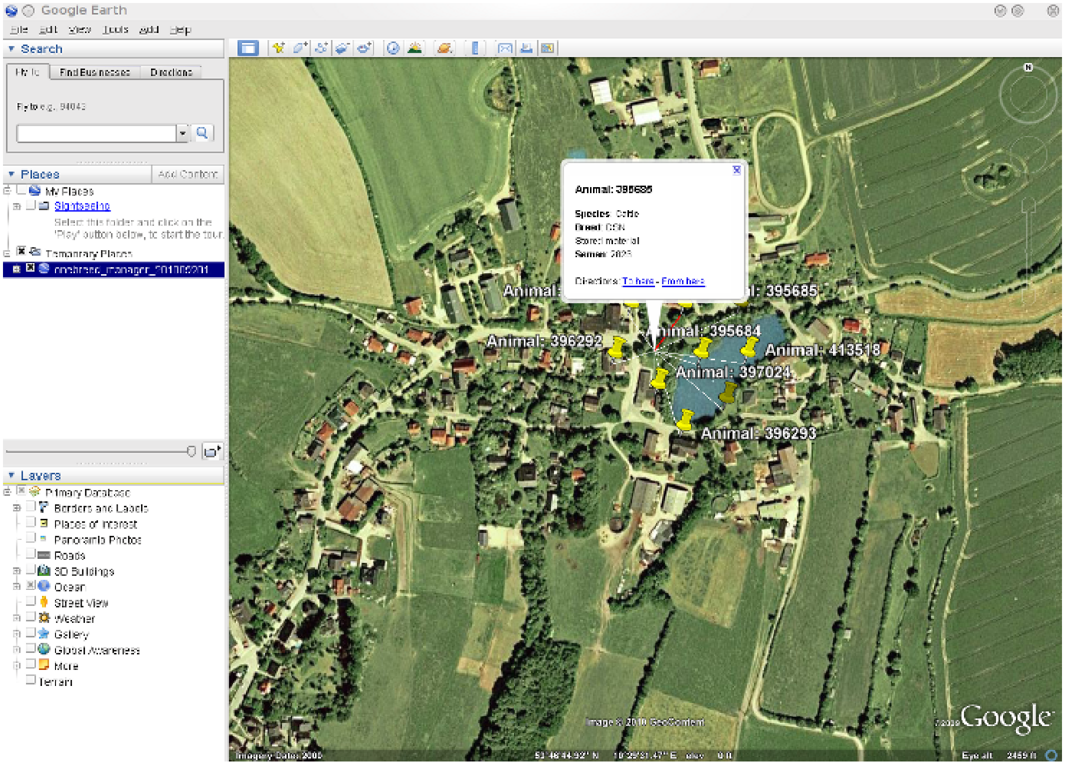
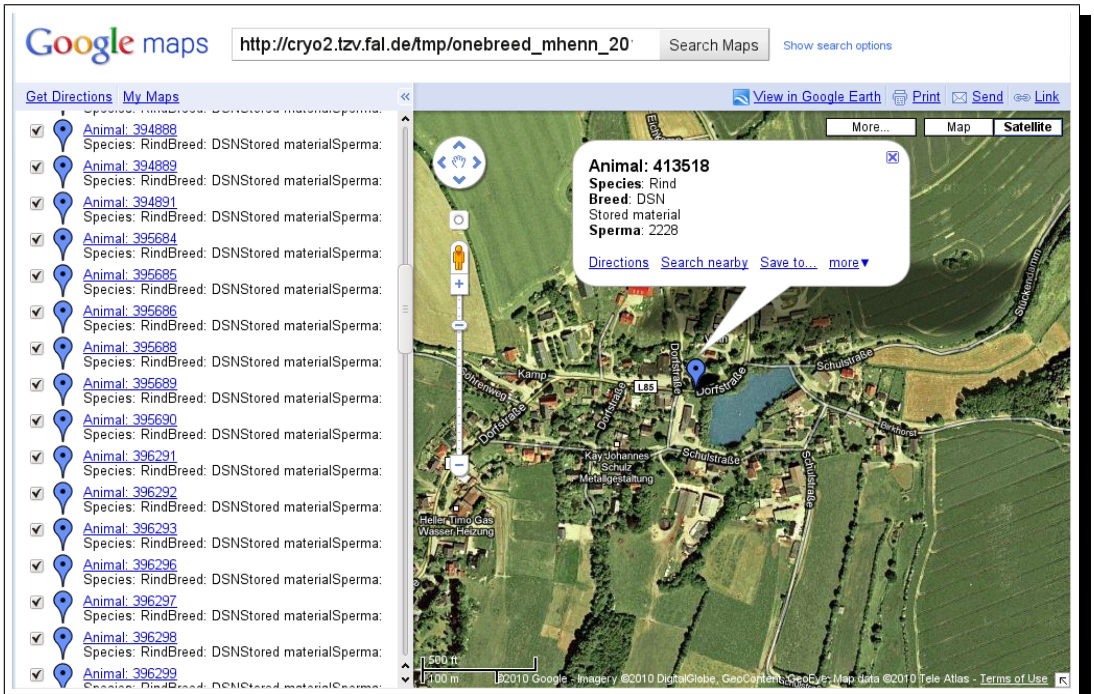


Figure 7.52: Visualization of the donors location in Google Earth

7.7.11 Exporting the location of donors from given breed for Google Maps

If the location coordinates of the animal donors were recorded, their distribution per breed can be visualized over the satellite imagery, maps and terrain offered by Google Earth. There the animal location along with the animal data and amount of stored material from that animal will be shown. As a prerequisite you should have the Google Earth software installed on your computer.

Open **Main Menu** ▷ **Reports** ▷ **Animals distribution**. Choose the species from the respective drop-down list. Wait until the breed list is populated and select the breed. Click the **Export data** link. When the file is generated, copy the link below **Copy the URL in Google Maps:**. Open the Google Maps web page (http://maps.google.com) in another browser window and paste the copied link in field in front of the **Search Maps** button. Click the **Search Maps** button. The animals will be shown on the map and listed in the **Contents** list as shown in Figure 7.53.



☑ Animal: 394888
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 394889
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 394891
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 395684
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 395685
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 395686
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 395688
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 395689
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 395690
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 396291
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 396292
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 396293
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 396296
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 396297
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 396298
Species: RindBreed: DSNStored materialSperma:
☑ Animal: 396299

Animal: 413518
Species: Rind
Breed: DSN
Stored material
Sperma: 2228

Figure 7.53: Visualization of the donors location in Google Maps

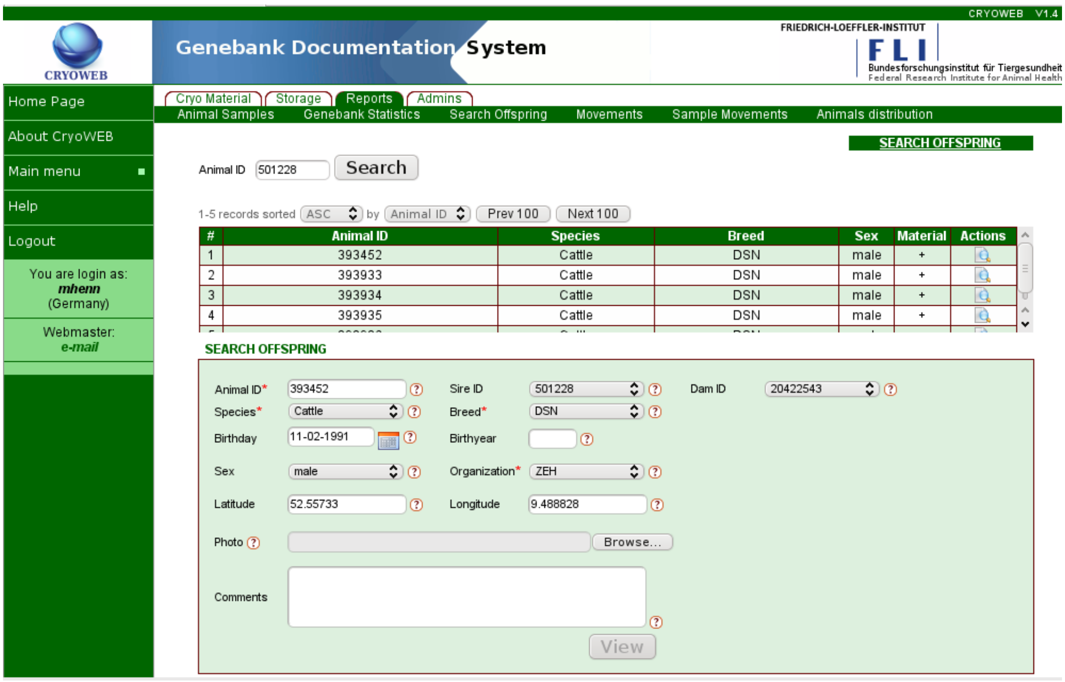
> **Note:** The link generated by CryoWEB expires after some time, and in this case you have to generate the report again and copy the new link to Google Maps.

7.7.12 Searching for offspring from a certain animal

Sometime you will be asked for material from the offspring from a certain animal. For this purpose in CryoWEB there is a form, allowing you to search by a animal number for direct offspring.

Open **Main Menu** ▷ **Reports** ▷ **Search Offspring.** Enter the **Animal ID** into the first field of the search part. Click the **Search** button. All animals, which are direct descendant from the searched one, will be listed in the results table. The donor animals are marked with '+' in the column Material (Figure 7.54).

To view the details of a certain offspring animal click on the View icon in the **Actions** section of the line containing the chosen Animal ID. The submit button label should change to **View**. The data for this animal will be shown in the **Search offspring** form below.



Animal ID 501228

1-5 records sorted ASC by Animal ID

#	Animal ID	Species	Breed	Sex	Material	Actions
1	393452	Cattle	DSN	male	+	
2	393933	Cattle	DSN	male	+	
3	393934	Cattle	DSN	male	+	
4	393935	Cattle	DSN	male	+	

Animal ID*	393452	Sire ID	501228	Dam ID	20422543
Species*	Cattle	Breed*	DSN		
Birthday	11-02-1991	Birthyear			
Sex	male	Organization*	ZEH		
Latitude	52.55733	Longitude	9.488828		
Photo					
Comments					

Figure 7.54: Searching for offspring from animal 501228

8 Administrator's tasks

The administrator's tasks can be divided in two separate groups - management of drop-down lists items and management of the CryoWEB users accounts.

The first group contains the management of the items for the drop-down lists on the CryoWEB page, which are used by all users for data entry and retrieval. These include inter alia management of species and breeds lists, vessel types, country names. If a user wants to enter a donor from a breed which is not already present in the local installation, she must ask the administrator to register first this breed in CryoWEB.

The tasks in this group are carried out via the **Admins** tab in the CryoWEB page. To access the **Admins** menu go to **Main menu** ▷ **Admins** tab.

The second group of tasks encompasses the management of the user accounts. These includes, e.g. registering new user in the system, assigning privileges to an user, blocking user from accessing the system, etc. As all genebank information in CryoWEB is hidden from the general public, only registered users who have an account in CryoWEB can view or modify the data.

The tasks in this group are carried out via the **Access Rights Manager** (**ARM**) web page which comes together with the CryoWEB installation.

For all administrative tasks you have to be logged in the respective page as user with administrator rights.

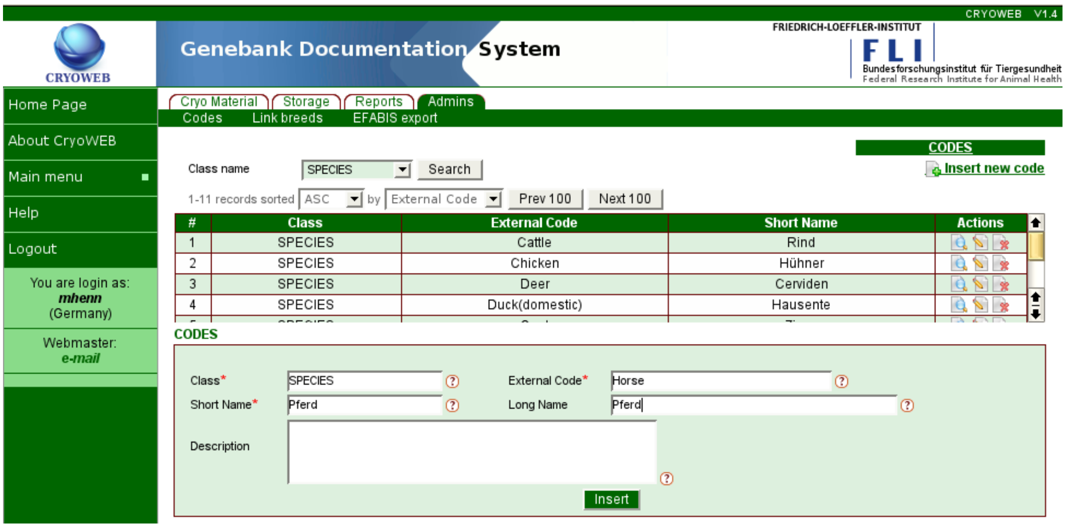
8.1 Breeds and species management

In this section you will learn how to add new species and breed names, how to link breed names to various species and link the breed names used in CryoWEB to the ones registered in EFABIS.

8.1.1 Adding new species

To add a new species click on **Admins** ▷ **Codes**. From the drop-down list **Class name**, choose the option **SPECIES** and press the **Search** button.

If there are any species registered in the database they will be listed below. If your species name is not in the database, click on **Insert new code** to start filling the data for it. In the **Codes** form below the list, the system will fill for you automatically the class as **SPECIES**, and this value cannot be changed.



Class name: SPECIES

1-11 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	SPECIES	Cattle	Rind	
2	SPECIES	Chicken	Hühner	
3	SPECIES	Deer	Cerviden	
4	SPECIES	Duck(domestic)	Hausente	

CODES

Class*: SPECIES

External Code*: Horse

Short Name*: Pferd

Long Name: Pferd

Description:

Figure 8.1: Adding new species - Horse

Enter in the **External Code** field a short English name for the species. Enter in the **Short Name** field the species name, the way you want to see it in the drop-down lists in CryoWEB, e.g. in your local language, or abbreviated. You must add a long name for the species (will be used in the reports), and optionally, a description in the respective fields as it is shown in Figure 8.1.

To enter the new species into the database, click the **Insert** button. If the insert was successful the new species will be listed above the **Codes** form.

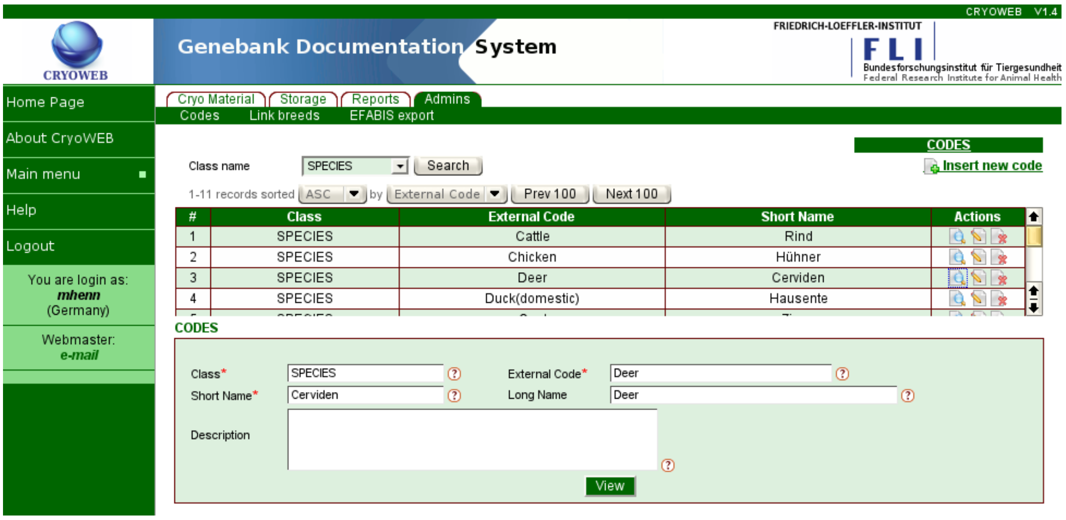
8.1.2 Viewing species data

Open **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **SPECIES**, and click the **Search** button.

The list of all species names registered in the database is shown in the search results table in groups of 100. These summaries include the **External Code** and the **Short Name** of the species.

To view the complete data for certain species, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the species name you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the species will be shown in the **Codes** form below (Figure 8.2).



Class name: SPECIES

1-11 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	SPECIES	Cattle	Rind	
2	SPECIES	Chicken	Hühner	
3	SPECIES	Deer	Cerviden	
4	SPECIES	Duck(domestic)	Hausente	

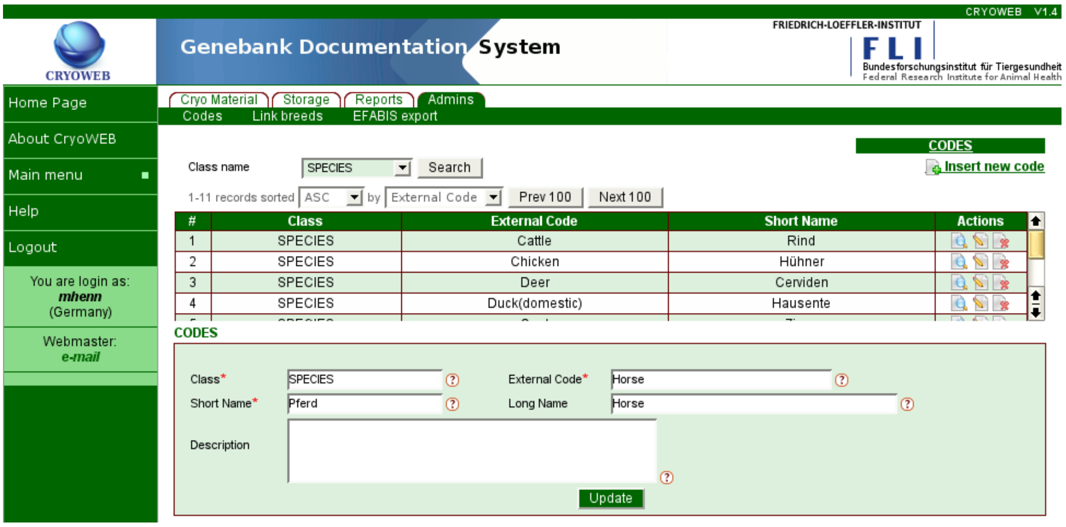
CODES

Class*: SPECIES
External Code*: Deer
Short Name*: Cerviden
Long Name: Deer
Description:

Figure 8.2: View species data

8.1.3 Correcting species name

To change species name click on **Admins** ▷ **Codes**. From the drop-down list **Class** choose the option **SPECIES** and click the **Search** button.



Class name: SPECIES

1-11 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	SPECIES	Cattle	Rind	
2	SPECIES	Chicken	Hühner	
3	SPECIES	Deer	Cerviden	
4	SPECIES	Duck(domestic)	Hausente	

CODES

Class*: SPECIES
External Code*: Horse
Short Name*: Pferd
Long Name: Horse
Description:

Figure 8.3: Correcting the species name Horse

In the result list below find the line containing the species and click the **Update** (middle) icon in the **Actions** section of this line. The data for the species will be shown in the **Codes** form below.

Make your corrections in the respective form fields (Figure 8.3) and click the **Update** button in the bottom of the form to submit the changes to the database.

To check if the changes were successfully submitted, find the line in the list containing the species, and click the **View** (left) icon in the **Actions** section of that line. The data in the **Codes** form will be re-read from the database.

8.1.4 Deleting species

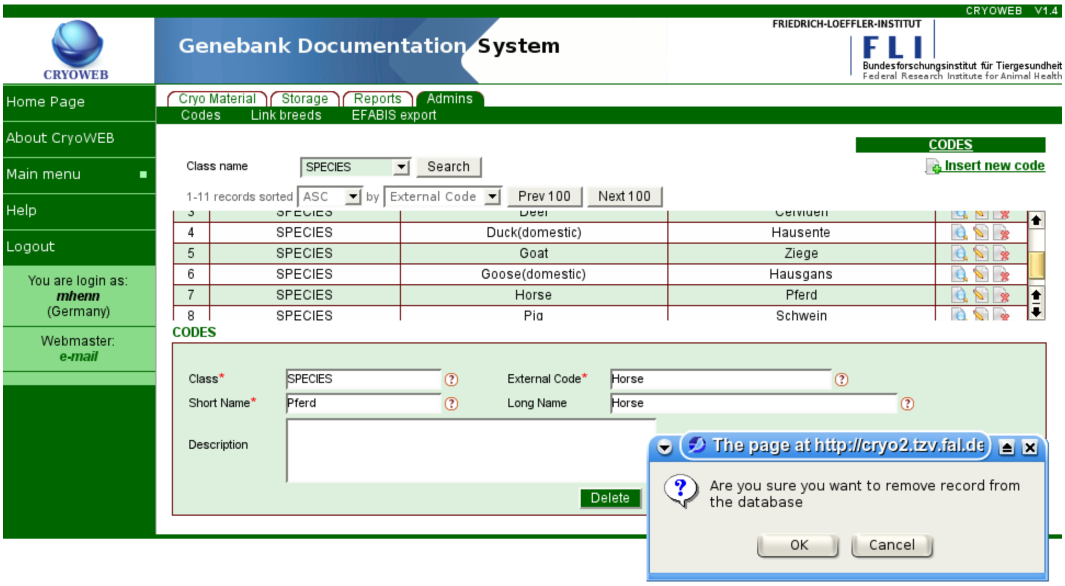
To delete a species name, it must not be used, i.e. there should be no link between the species and any breeds, and there should be no animals from this species in the database.

If the species is not used click on **Admins**▷**Codes**. From the drop-down list **Class** choose the option **SPECIES** and click the **Search** button. In the list below find the line containing the species and click the **Delete** (right) icon in the **Actions** section of this line. The data for these species will be shown in the **Codes** form below.

To erase the species click on the **Delete** button in the bottom of the form (Figure 8.4). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**.



Class name: SPECIES

1-11 records sorted ASC by External Code

4	SPECIES	Duck(domestic)	Hausente
5	SPECIES	Goat	Ziege
6	SPECIES	Goose(domestic)	Hausgans
7	SPECIES	Horse	Pferd
8	SPECIES	Pig	Schwein

CODES

Class*: SPECIES

External Code*: Horse

Short Name*: Pferd

Long Name: Horse

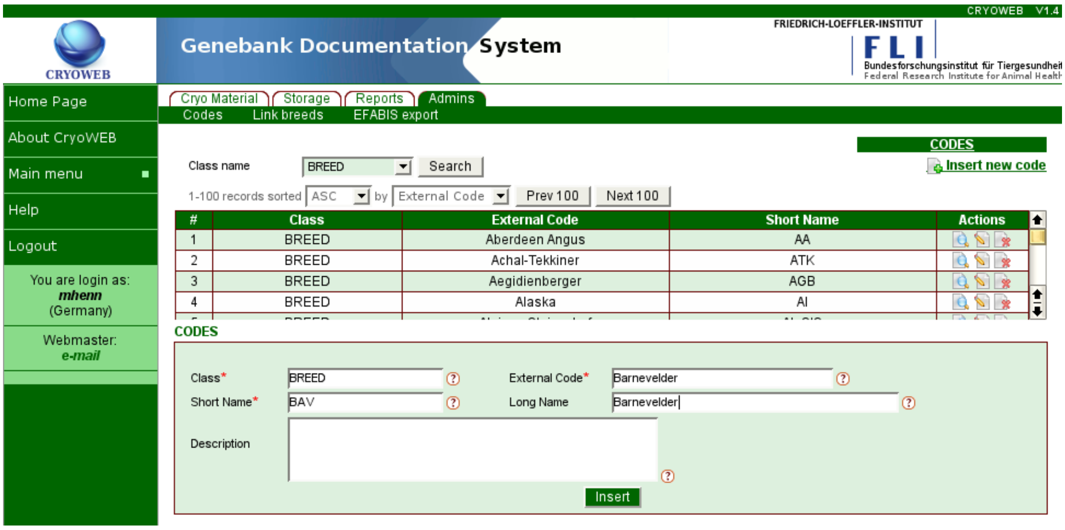
Description:

Are you sure you want to remove record from the database

Figure 8.4: Deleting the species name Horse

8.1.5 Adding new breed

To add a new breed click on **Admins** ▷ **Codes**. From the drop-down list **Class** name choose the option **BREED**, and click the **Search** button.



Class name: BREED

1-100 records sorted ASC by External Code

#	Class	External Code	Short Name
1	BREED	Aberdeen Angus	AA
2	BREED	Achal-Tekkiner	ATK
3	BREED	Aegidienberger	AGB
4	BREED	Alaska	AI

CODES

Class*: BREED

External Code*: Barnevelder

Short Name*: BAV

Long Name: Barnevelder

Description:

Figure 8.5: Adding a new breed name Barnevelder

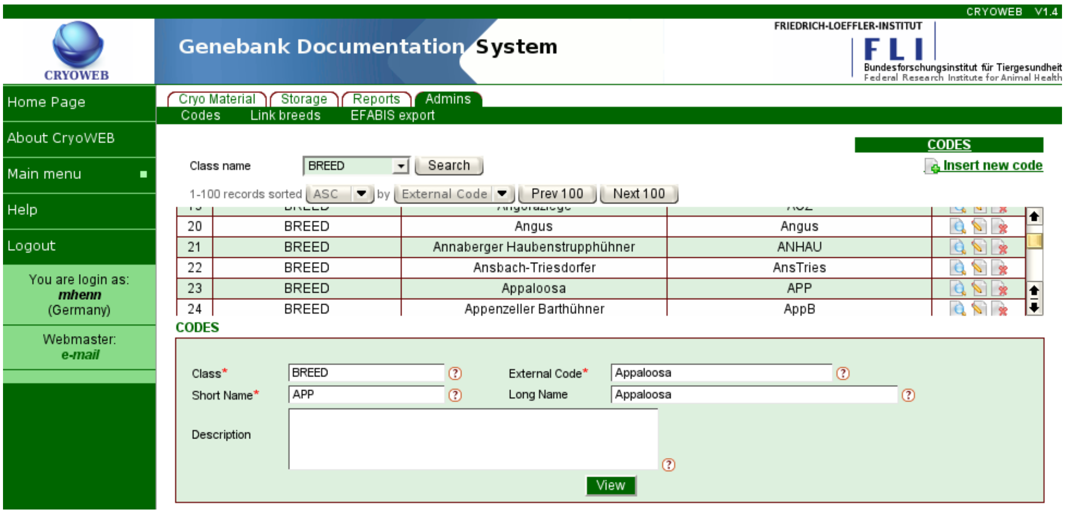
If there are any breeds registered in the database they will be listed below. If the breed name is not in the database, click on **Insert new code** to start filling the data for the breed. In the **Codes** form below the list, the system will fill for you automatically the class as **BREED**, and this value cannot be changed.

Enter in the **External Code** field a short English name for the breed. Enter in the **Short Name** field the breed name the way you want to see it in the drop-down lists in CryoWEB, e.g. in your local language, or abbreviated (Figure 8.5). You must add a long name for the breed (will be used in the reports) and, optionally, a description in the respective fields.

To enter the new breed in the database, click the **Insert** button. If the insert was successful, the new breed will be listed above the **Codes** form.

8.1.6 Viewing breed data

Open **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **BREED**, and click the **Search** button.



Class name: BREED

1-100 records sorted ASC by External Code

20	BREED	Angus	Angus
21	BREED	Annaberger Haubenstrupphühner	ANHAU
22	BREED	Ansbach-Triesdorfer	AnsTries
23	BREED	Appaloosa	APP
24	BREED	Appenzeller Barthühner	AppB

CODES

Class*: BREED

External Code*: Appaloosa

Short Name*: APP

Long Name: Appaloosa

Description:

Figure 8.6: View breed data

The list of all breed names registered in the database is shown in the search results table in groups of 100. These summaries include the **External Code** and the **Short Name** of the breeds.

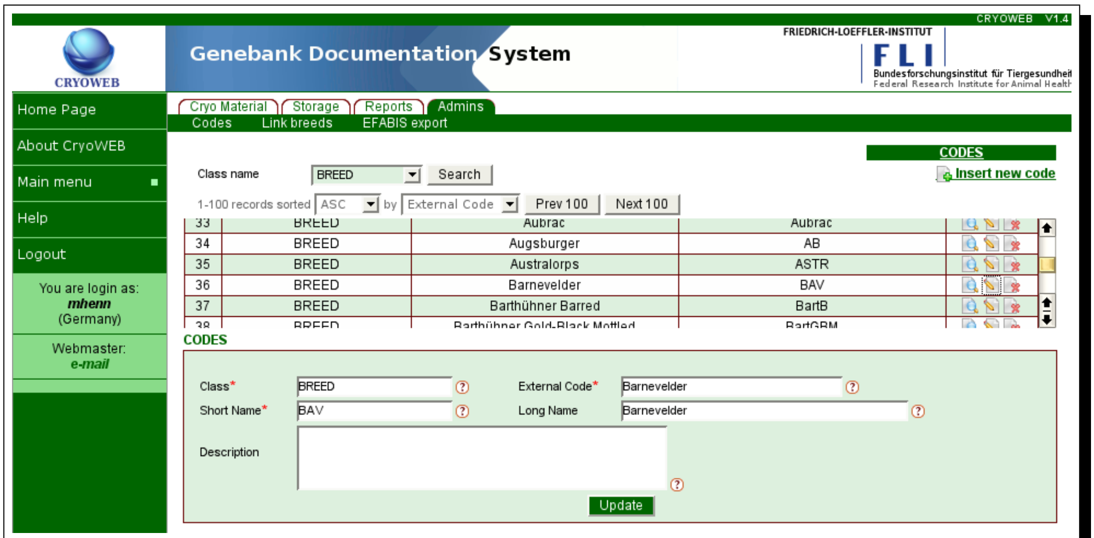
To view the complete data for a certain breed, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the breed name you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the breed will be shown in the **Codes** form below (Figure 8.6).

8.1.7 Correcting a breed name

To correct a breed name, click on **Admins** ▷ **Codes**.

From the drop-down list **Class** choose the option **BREED**, and click the **Search** button. In the list below find the line containing the breed name, and click the **Update** (middle) icon in the **Actions** section of this line. The data for the breed will be shown in the **Codes** form below.



Class name: BREED

1-100 records sorted ASC by External Code

33	BREED	Aubrac	Aubrac
34	BREED	Augsburger	AB
35	BREED	Australorps	ASTR
36	BREED	Barnevelder	BAV
37	BREED	Barthühner Barred	BartB
38	BREED	Barthühner Gold-Black Mottled	BartGBM

Class*: BREED
External Code*: Barnevelder
Short Name*: BAV
Long Name: Barnevelder
Description:

Figure 8.7: Correcting a breed name

Make your corrections in the respective form fields, and click the **Update** button in the bottom of the form to submit the changes to the database (Figure 8.7).

To check that the changes were successfully submitted, find the line in the list containing the breed, and click the **View** (left) icon in the **Actions** section of that line. The data in the **Codes** form will be re-read from the database.

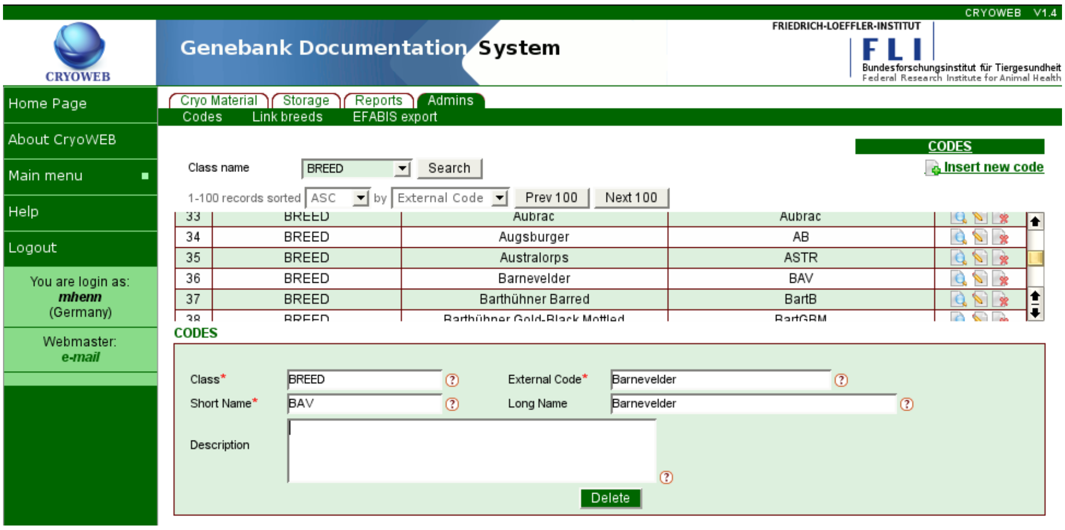
8.1.8 Deleting a breed

You can only delete breed name which is not used, i.e. the breed must be not linked to species, and there must be no animals from this breed in the database. Therefore, before deleting a breed you must delete all animals from that breed and the links to any species.

If the breed name is not used, click on **Admins** ▷ **Codes**. From the drop-down list **Class**, choose the option **BREED**, and click the **Search** button. In the list below find the line containing the breed, and click the **Delete** (right) icon in the **Actions** section of this line. The data for the breed will be shown in the **Codes** form below (Figure 8.8). To erase the breed click on the **Delete** button in the bottom of the form. A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**.



Class name: BREED

1-100 records sorted ASC by External Code

33	BREED	Aubrac	Aubrac
34	BREED	Augsburger	AB
35	BREED	Australorps	ASTR
36	BREED	Barnevelder	BAV
37	BREED	Barthühner Barred	BartB
38	BREED	Barthühner Gold-Black Mottled	BartGBM

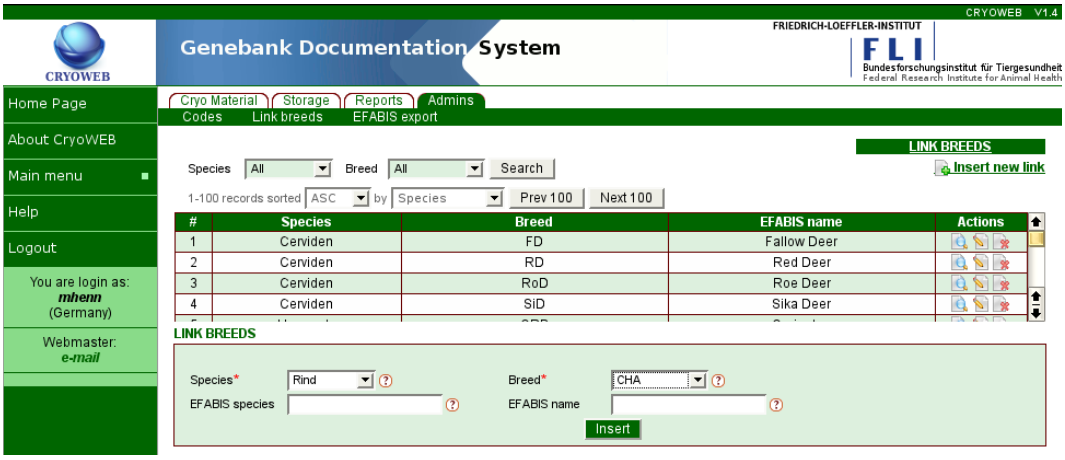
CODES

Class*: BREED
External Code*: Barnevelder
Short Name*: BAV
Long Name: Barnevelder
Description:

Figure 8.8: Deleting the breed name Barnevelder

8.1.9 Linking breed name to species

On the breed's form, the breed's list is filtered by the species name. To make this possible you have to link each breed to the respective species, i.e. assign the breed to a species.



Species: All
Breed: All

1-100 records sorted ASC by Species

#	Species	Breed	EFABIS name	Actions
1	Cerviden	FD	Fallow Deer	
2	Cerviden	RD	Red Deer	
3	Cerviden	RoD	Roe Deer	
4	Cerviden	SiD	Sika Deer	

LINK BREEDS

Species*: Rind
Breed*: CHA
EFABIS species:
EFABIS name:

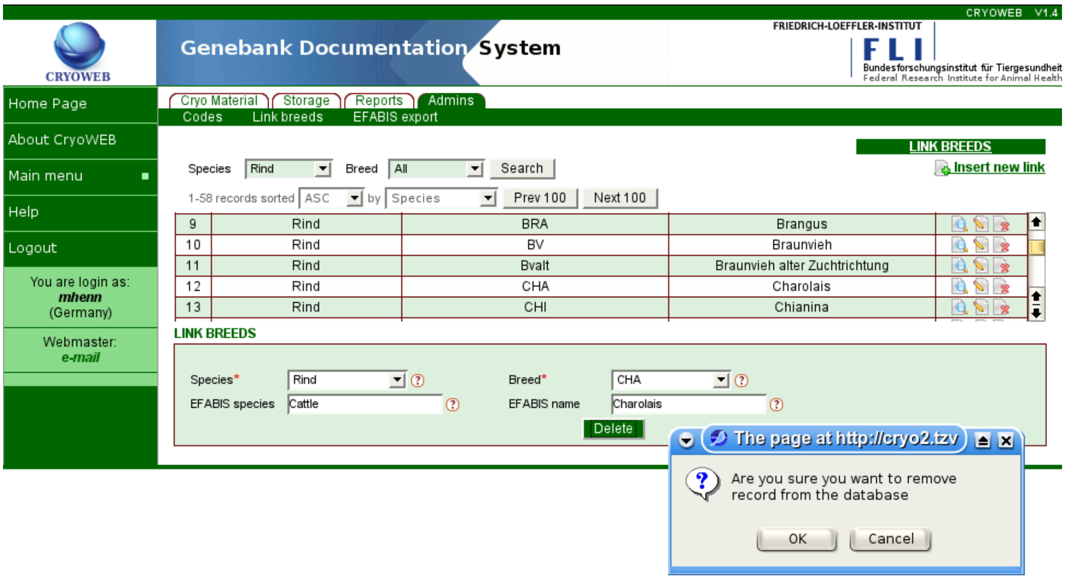
Figure 8.9: Linking breed name CHA and species Rind

To link breed and species names, click on **Admins**▷**Link breeds**. Then choose from the **Species** list in the search part the name of the species you want to link the breed, and click the **Search** button. Check if your breed is in the results list. If this is not the case, click on the **Insert new link** icon, choose the species and breed name from the respective drop-down lists on the **Link Breeds** form, and click the **Insert** button. If the linking was successful, you can find the new record in the table above. In the Figure 8.9 the breed CHA is linked to the species 'Rind'.

8.1.10 Deleting a link between breed name and species

To delete a link between CryoWEB breed name and species, click on the **Admins** ▷ **Link breeds**. Find the respective line in the list, and click the **Delete** (right) icon in the **Actions** section of this line. The link data will be shown in the **Link breeds** form below. To erase the links, click on the **Delete** button in the bottom of the form (Figure 8.10).

> **Warning:** If there are any animals from that breed registered in the database, they will not be erased. However, you cannot update their data, or add new animals from that breed until the link is restored.



You are login as: **mhenn** (Germany)

Species: Rind
Breed: All

1-58 records sorted ASC by Species

9	Rind	BRA	Brangus
10	Rind	BV	Braunvieh
11	Rind	Bvalt	Braunvieh alter Zuchtrichtung
12	Rind	CHA	Charolais
13	Rind	CHI	Chianina

LINK BREEDS

Species*: Rind
Breed*: CHA
EFABIS species: Cattle
EFABIS name: Charolais

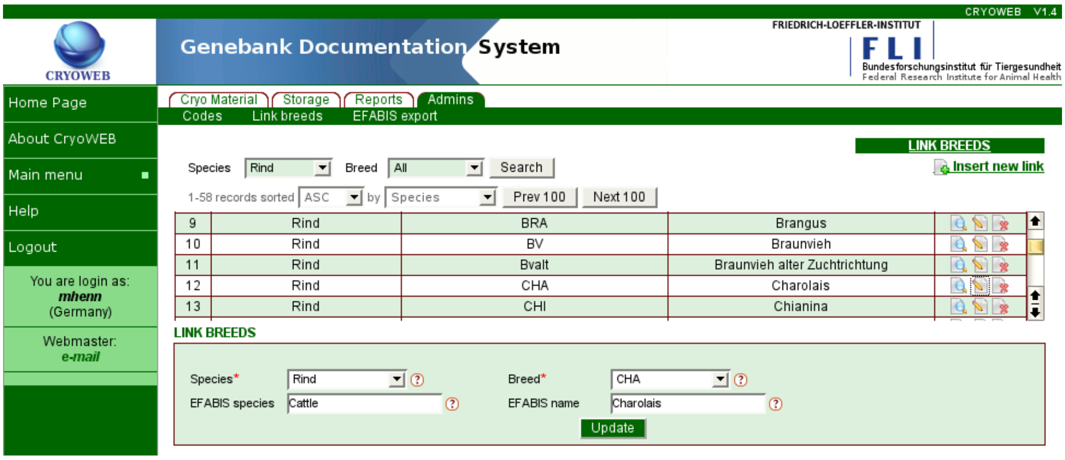
The page at http://cryo2.tzv

Are you sure you want to remove record from the database

Figure 8.10: Deleting link between breed name and species

8.1.11 Linking CryoWEB breed name to EFABIS breed name

The breed names used in CryoWEB may differ from the ones in EFABIS (as the breeds have sometimes more than one name). If you want to get cumulative statistics per breed from CryoWEB for upload in EFABIS, you have to link the names used in both systems.



Species: Rind
Breed: All
1-58 records sorted ASC by Species

9	Rind	BRA	Brangus
10	Rind	BV	Braunvieh
11	Rind	Bvalt	Braunvieh alter Zuchtrichtung
12	Rind	CHA	Charolais
13	Rind	CHI	Chianina

LINK BREEDS

Species*: Rind
Breed*: CHA
EFABIS species: Cattle
EFABIS name: Charolais

Figure 8.11: Linking CryoWEB breed name for Charolais to EFABIS breed name

To link CryoWEB and EFABIS names, click on the **Admins** ▷ **Link breeds**.

If the CryoWEB breed name is not linked to species, click on the Insert new link icon, choose the CryoWEB species and breed name from the respective drop-down lists on the **Link breeds** form, type the EFABIS species and breed name in the text fields below, and click the **Insert** button.

If the CryoWEB breed name is linked to species, find the respective line in the list, and click the **Update** (middle) icon in the **Actions** section of this line. Type the EFABIS species and breed name in the text fields in the **Link breeds** form, and click the **Update** button (Figure 8.11).

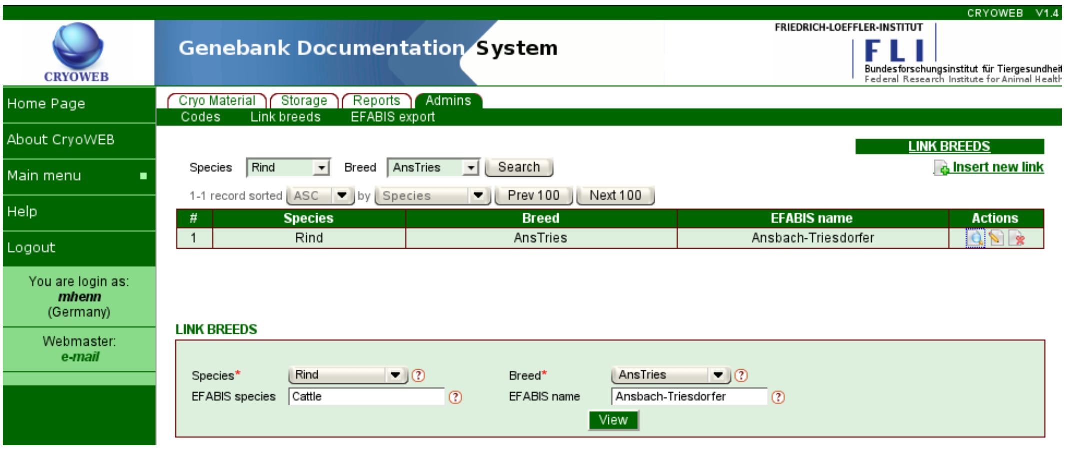
8.1.12 Viewing links data

To view a link data click on the **Admins** ▷ **Link breeds**.

The list of all links between breeds and species registered in the database is shown in the search results table in groups of 100. These summaries include the species, the CryoWEB name and the EFABIS name of the linked breed.

To view the complete data for a certain link, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the breed name, which link you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the link will be shown in the **Link breeds** form below (Figure 8.12).



You are login as: **mhenn** (Germany)

Webmaster: *e-mail*

Species: Rind Breed: AnsTries

1-1 record sorted ASC by Species

#	Species	Breed	EFABIS name	Actions
1	Rind	AnsTries	Ansbach-Triesdorfer	

LINK BREEDS

Species*: Rind

Breed*: AnsTries

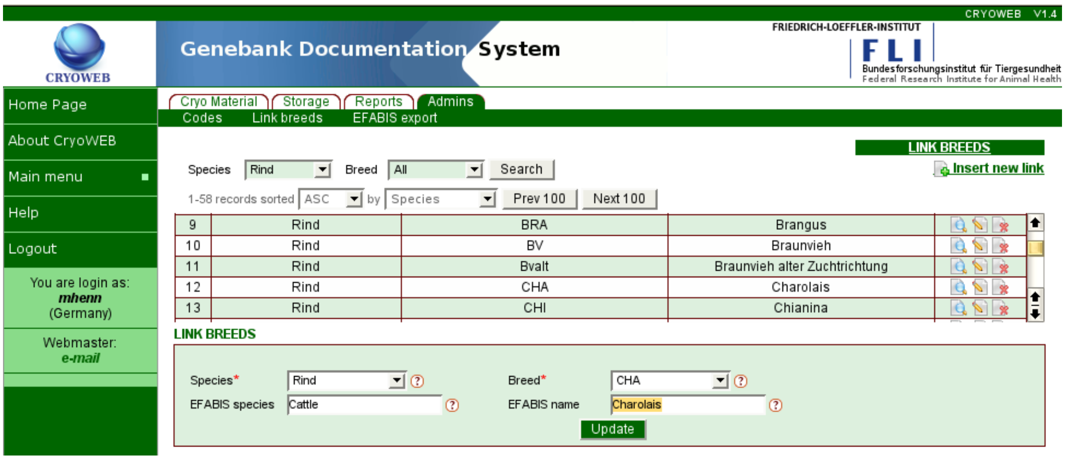
EFABIS species: Cattle

EFABIS name: Ansbach-Triesdorfer

Figure 8.12: View links data

8.1.13 Correcting a link between CryoWEB and EFABIS breed names

To correct a link click on **Admins** ▷ **Link breeds**. Find the respective line in the list, and click the **Update** (middle) icon in the **Actions** section of this line. The link data will be shown in the **Link breeds** form below. Correct the EFABIS breed name or species, and click the **Update** button (Figure 8.13).



You are login as: **mhenn** (Germany)

Webmaster: *e-mail*

Species: Rind Breed: All

1-58 records sorted ASC by Species

9	Rind	BRA	Brangus	
10	Rind	BV	Braunvieh	
11	Rind	Bvalt	Braunvieh alter Zuchtrichtung	
12	Rind	CHA	Charolais	
13	Rind	CHI	Chianina	

LINK BREEDS

Species*: Rind

Breed*: CHA

EFABIS species: Cattle

EFABIS name: Charolais

Figure 8.13: Correcting link between the CryoWEB and EFABIS name for Charolais breed

8.2 Vessel type management

In this section you will learn how to add and remove various types of vessels.

8.2.1 Adding a new vessel type

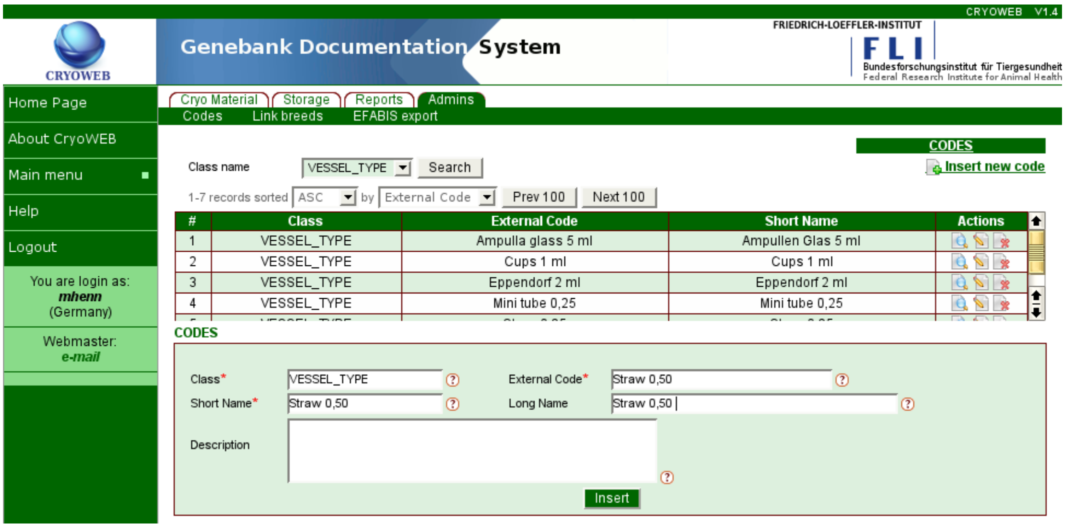
To add a new vesseltype, click on **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **VESSEL_TYPE** and click the **Search** button.

If there are any vessel types registered in the database, they will be listed below. Check if this type is not already in the database.

If the vessel type is not in the database, click on the **Insert new code** to start filling the data for it. In the **Codes** form below the list, the system will fill for you automatically the class as **VESSEL_TYPE**, and this value cannot be changed.

Enter in the **External Code** field a short English name for the vessel type. Enter in the **Short Name** field the vessel type, the way you want to see it in the drop-down lists in CryoWEB, e.g. in your local language, or abbreviated. You must add also long name for this type and, optionally, a description in the respective fields.

To enter the new type in the database, click the **Insert** button (Figure 8.14). If the insert was successful the new vessel type will be listed above the **Codes** form.



Class name: VESSEL_TYPE

1-7 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	VESSEL_TYPE	Ampulla glass 5 ml	Ampullen Glas 5 ml	
2	VESSEL_TYPE	Cups 1 ml	Cups 1 ml	
3	VESSEL_TYPE	Eppendorf 2 ml	Eppendorf 2 ml	
4	VESSEL_TYPE	Mini tube 0,25	Mini tube 0,25	

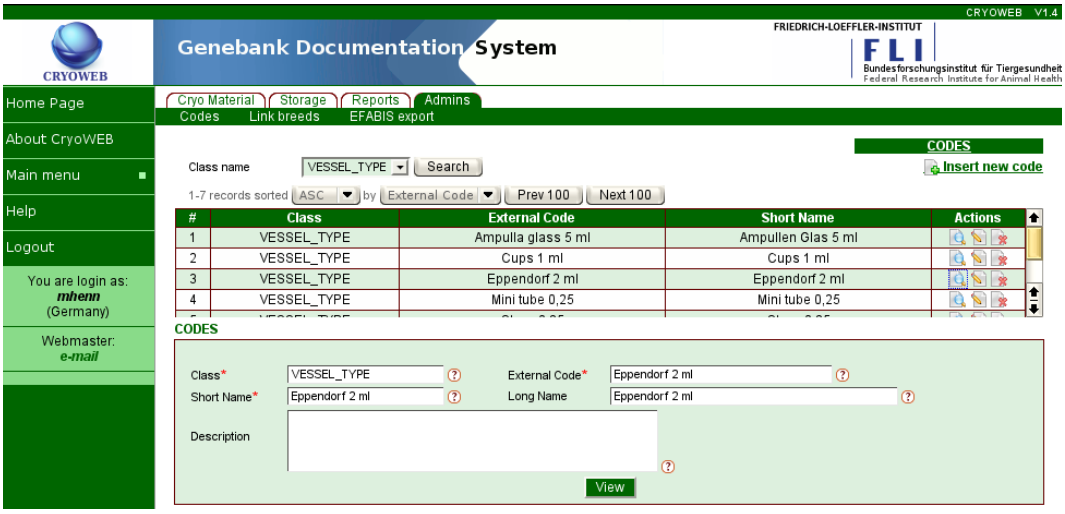
CODES

Class*: VESSEL_TYPE
External Code*: Straw 0,50
Short Name*: Straw 0,50
Long Name: Straw 0,50
Description:

Figure 8.14: Adding a new vessel type - “Straw 0.50”

8.2.2 Viewing vessel type data

Open **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **VESSEL_TYPE**, and click the **Search** button.



Class name VESSEL_TYPE

1-7 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	VESSEL_TYPE	Ampulla glass 5 ml	Ampullen Glas 5 ml	
2	VESSEL_TYPE	Cups 1 ml	Cups 1 ml	
3	VESSEL_TYPE	Eppendorf 2 ml	Eppendorf 2 ml	
4	VESSEL_TYPE	Mini tube 0,25	Mini tube 0,25	

CODES

Class* VESSEL_TYPE

External Code* Eppendorf 2 ml

Short Name* Eppendorf 2 ml

Long Name Eppendorf 2 ml

Description

Figure 8.15: View vessel type data

The list of all vessel types registered in the database is shown in the search results table in groups of 100. These summaries include the **External Code** and the **Short Name** of the type.

To view the complete data for a certain vessel type, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the type you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the vessel type will be shown in the **Codes** form below (Figure 8.15).

8.2.3 Deleting a vessel type

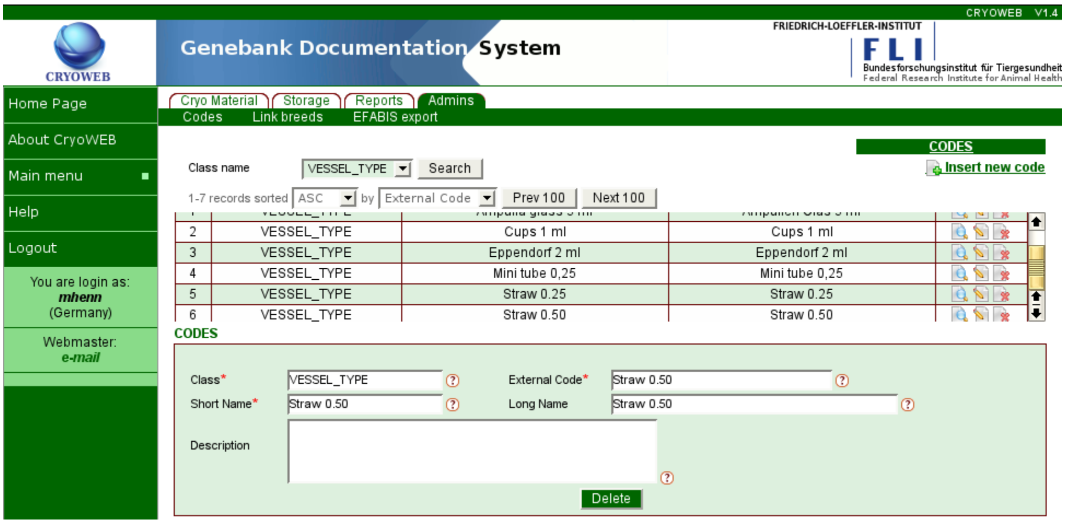
To delete a vessel type it must not be in use, i.e. there should be no samples packed in this vessel type in the database. Therefore, before deleting a vessel type, you must delete all samples stored in such vessels (if that is what you want to do).

If the vessel type is not used, click on **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **VESSEL_TYPE** and click the **Search** button. In the list below find the line containing the vessel type and click the **Delete** (right) icon in the **Actions** section of this line. The data for this type will be shown in the **Codes** form below.

To erase the vessel type, click on the **Delete** button in the bottom of the form (Figure 8.16). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**.



Class name: VESSEL_TYPE

1-7 records sorted ASC by External Code

2	VESSEL_TYPE	Cups 1 ml	Cups 1 ml
3	VESSEL_TYPE	Eppendorf 2 ml	Eppendorf 2 ml
4	VESSEL_TYPE	Mini tube 0,25	Mini tube 0,25
5	VESSEL_TYPE	Straw 0.25	Straw 0.25
6	VESSEL_TYPE	Straw 0.50	Straw 0.50

Class*: VESSEL_TYPE
External Code*: Straw 0.50
Short Name*: Straw 0.50
Long Name: Straw 0.50
Description:

Figure 8.16: Deleting the “Straw 0.50” vessel type

8.3 Material status types management

There are three predefined types for the legal status of the sample - **core**, **owned** and **free**. These can be renamed to fit the situation within the country.

8.3.1 Renaming a status type

To rename a status type, click on **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **AVAILABILITY**, and click the **Search** button.

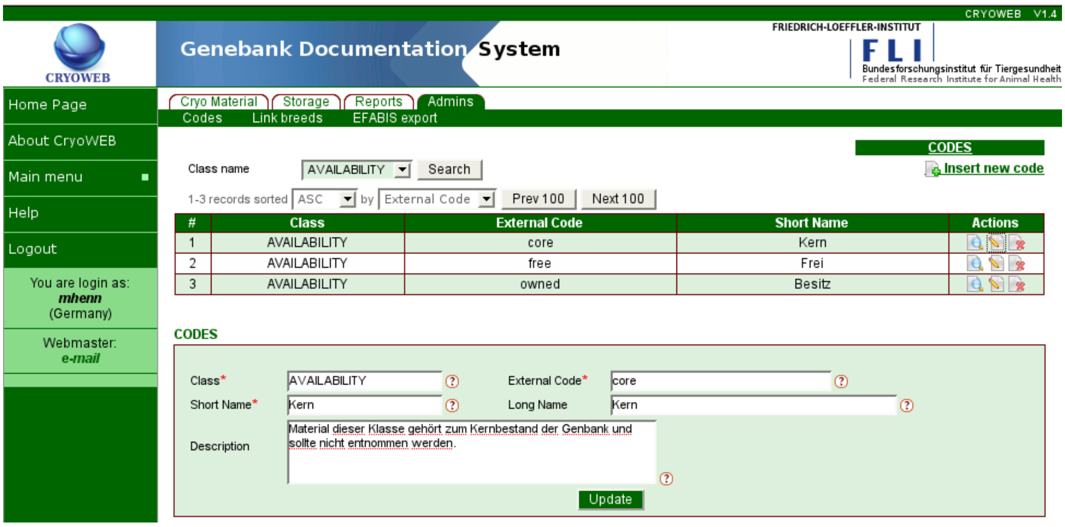
In the list below find the line containing the status type you want to rename, and click the **Update** (middle) icon in the **Actions** section of this line. The data for the status type will be shown in the **Codes** form below.

Make your corrections in the **Short name**, **Long name**, or **Description** fields, and click the **Update** button in the bottom of the form to submit the changes to the database (Figure 8.17).

Notice, that you must NOT change the external code for ’core’!

To check if the changes were successfully submitted, find the line in the list containing the status type, and click the **View** (left) icon in the **Actions** section of that line. The data in the **Codes** form will be re-read from the database.

> **Note:** You must not change the **External code** field for the predefined types - **core**, **owned** and **free**, as these values are used in the software.



Class name: AVAILABILITY

1-3 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	AVAILABILITY	core	Kern	
2	AVAILABILITY	free	Frei	
3	AVAILABILITY	owned	Besitz	

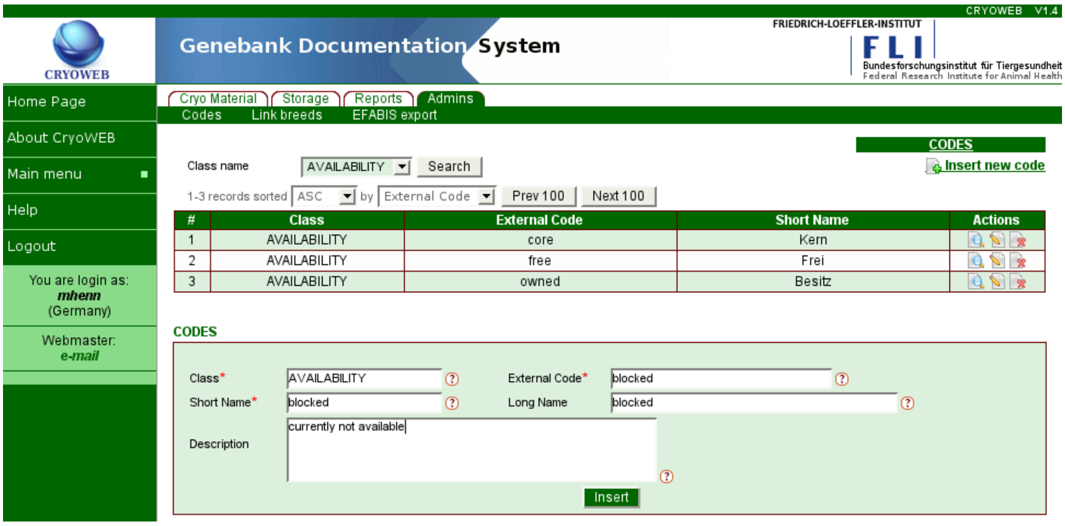
CODES

Class*: AVAILABILITY
External Code*: core
Short Name*: Kern
Long Name: Kern
Description: Material dieser Klasse gehört zum Kernbestand der Genbank und sollte nicht entnommen werden.

Figure 8.17: Renaming the core status type

8.3.2 Adding new status type

To add a new status type, click on **Admins ▷ Codes**. From the drop-down list **Class name** choose the option **AVAILABILITY**, and click the **Search** button.



Class name: AVAILABILITY

1-3 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	AVAILABILITY	core	Kern	
2	AVAILABILITY	free	Frei	
3	AVAILABILITY	owned	Besitz	

CODES

Class*: AVAILABILITY
External Code*: blocked
Short Name*: blocked
Long Name: blocked
Description: currently not available

Figure 8.18: Adding a new status - blocked

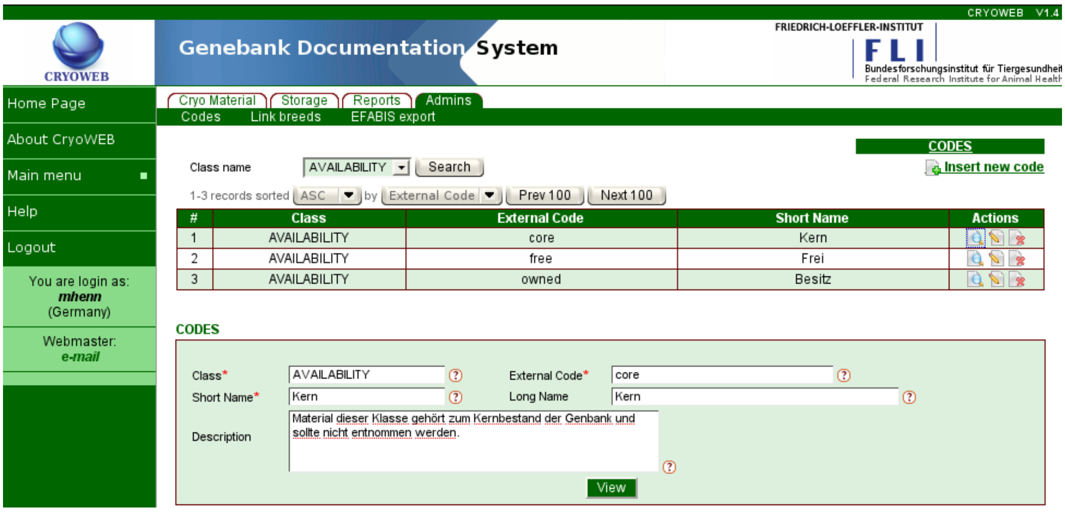
If the status type is not in the database, click on the **Insert new code**. In the **Codes** form below the list, the class will be fixed to **AVAILABILITY**.

Enter in the **External Code** field a short English name for the status type. Enter in the **Short Name** field the status name the way you want to see it in the drop-down lists in CryoWEB, e.g. in your local language, or abbreviated. You must add also a long name for the status type and, optionally, a description in the respective fields.

To enter the new status type in the database, click the **Insert** button (Figure 8.18). If the insert was successful, the new status will be listed above the **Codes** form.

8.3.3 Viewing status type data

Open **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **AVAILABILITY**, and click the **Search** button.



Class name: AVAILABILITY

1-3 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	AVAILABILITY	core	Kern	
2	AVAILABILITY	free	Frei	
3	AVAILABILITY	owned	Besitz	

CODES

Class*: AVAILABILITY
External Code*: core
Short Name*: Kern
Long Name: Kern
Description: Material dieser Klasse gehört zum Kernbestand der Genbank und sollte nicht entnommen werden.

Figure 8.19: View status type data

The list of all material status types registered in the database is shown in the search results table in groups of 100. These summaries include the **External Code** and the **Short Name** of the type.

To view the complete data for certain type, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the status type you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the status type will be shown in the **Codes** form below (Figure 8.19).

8.4 Exporting data for EFABIS

There is a network of national and regional information systems in Europe for monitoring and characterisation of all populations of domestic animals. The regional database in this network is called EFABIS - European Farm Animal Biodiversity Information System. EFABIS collects, inter alia, data about the in situ and ex situ conservation programmes, and in particular the amount of cryo-preserved genetic material per breed per year. The data is expected as plain text file in the following format:

```
Year|Breed|Species|Country|Semen|Embryos|Oocytes|Somatic cells(male)|Somatic cells(female)
```

In this regard CryoWEB can be used as a source for providing such information, by aggregating the single animal data and generating cumulative statistics per breed, material type and year. To generate such a file, click on **Admins** ▷ **EFABIS** export. Select from the list the years, for which you want to export data (Figure 8.20). Click on **Export data** to generate the file, then click on **Download:DS33.dat** to save the file to your machine. The generated file contains one line for each breed and year with the number of semen straws, embryos, oocytes, male and female somatic cells available in the storage in this year, and can be post-processed and uploaded in EFABIS.

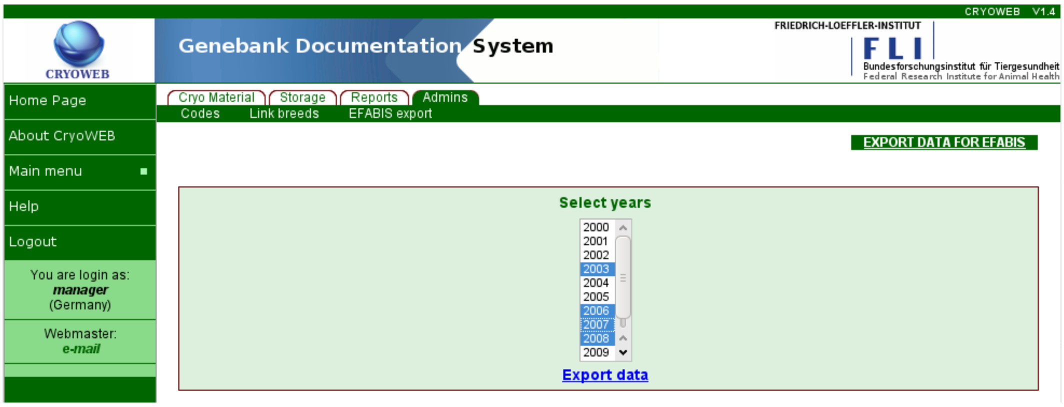


Figure 8.20: Selecting years to export

Note: This option might be used for tracing the development of your genebank collection in time.

8.5 Countries list management

In this section you will learn how to add, correct and remove country names from the list used on the **Organization** form.

8.5.1 Adding a new country

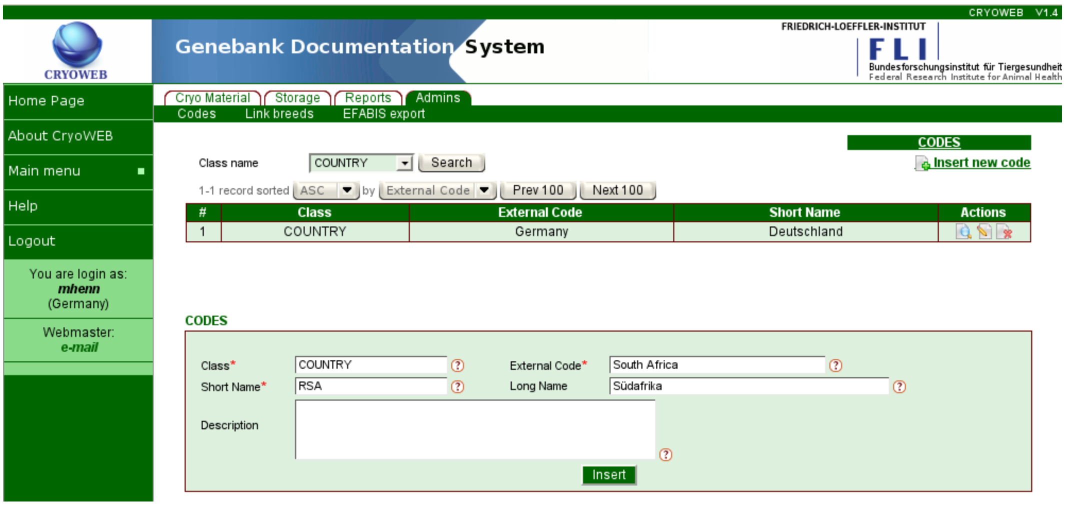
To add a new country, click on **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **COUNTRY** and click the **Search** button.

If there are any countries registered in the database, they will be listed below. Check if the country name is not already in the database.

If the country name is not in the database, click on the **Insert new code** to start filling the data for it. In the **Codes** form below the list, the system will fill for you automatically the class as **COUNTRY**, and this value cannot be changed.

Enter in the **External Code** field the English name of the country, or the ISO 3166-1 country code. Enter in the **Short Name** field the country name, the way you want to see it in the drop-down lists in CryoWEB, e.g. in your local language, or abbreviated. You must add also long name for this country and, optionally, a description in the respective fields.

To enter the new country in the database, click the **Insert** button (Figure 8.21). If the insert was successful the new country name will be listed above the **Codes** form (if there are many countries registered you may need to scroll the list).



Class name: COUNTRY

1-1 record sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	COUNTRY	Germany	Deutschland	

CODES

Class*: COUNTRY

External Code*: South Africa

Short Name*: RSA

Long Name: Südafrika

Description:

Figure 8.21: Adding a new country name - “South Africa”

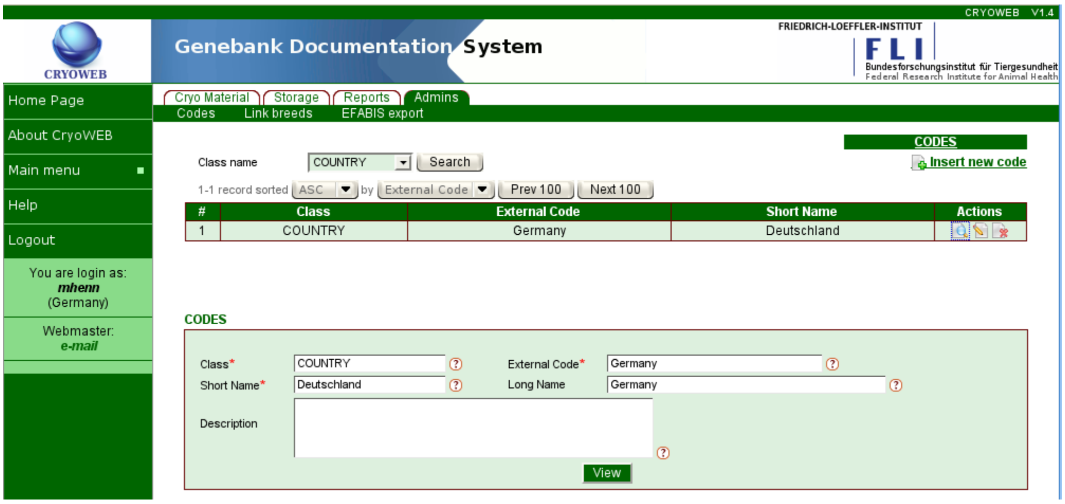
8.5.2 Viewing country data

Open **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **COUNTRY**, and click the **Search** button.

The list of all country names registered in the database is shown in the search results table in groups of 100. These summaries include the **External Code** and the **Short Name** of the country.

To view the complete data for a certain country, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the country name you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the country name will be shown in the **Codes** form below (Figure 8.22).



Class name: COUNTRY

1-1 record sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	COUNTRY	Germany	Deutschland	

CODES

Class*: COUNTRY

External Code*: Germany

Short Name*: Deutschland

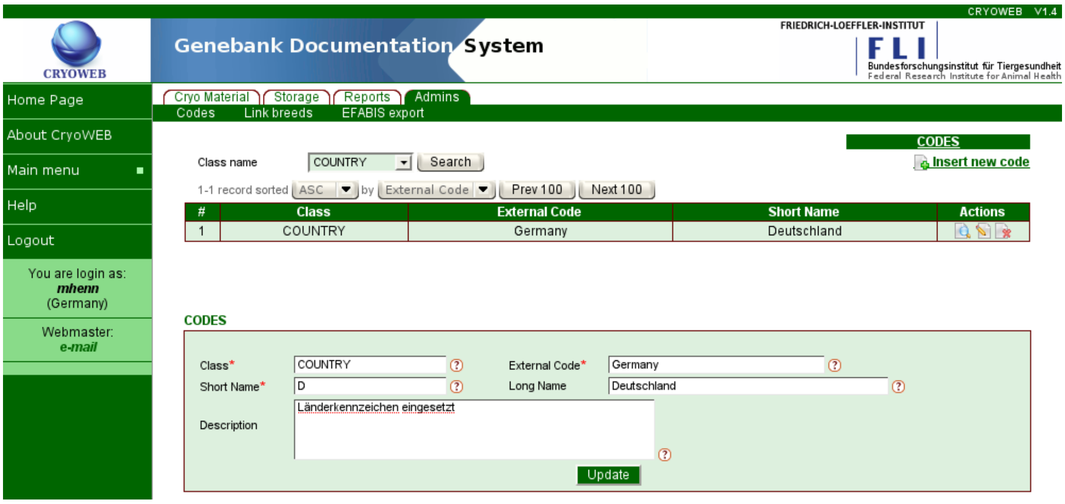
Long Name: Germany

Description:

Figure 8.22: View country data

8.5.3 Correcting country data

To correct a country name, click on **Admins ▷ Codes**.



Class name: COUNTRY

1-1 record sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	COUNTRY	Germany	Deutschland	

CODES

Class*: COUNTRY

External Code*: Germany

Short Name*: D

Long Name: Deutschland

Description: Länderkennzeichen eingesetzt

Figure 8.23: Correcting a country name

From the drop-down list **Class** choose the option **COUNTRY**, and click the **Search** button. In the list below find the line containing the country name, and click the **Update** (middle) icon in the **Actions** section of this line. The data for the country will be shown in the **Codes** form below.

Make your corrections in the respective form fields, and click the **Update** button in the bottom of the form to submit the changes to the database (Figure 8.23).

To check that the changes were successfully submitted, find the line in the list containing the country, and click the **View** (left) icon in the **Actions** section of that line. The data in the **Codes** form will be re-read from the database.

8.5.4 Deleting a country

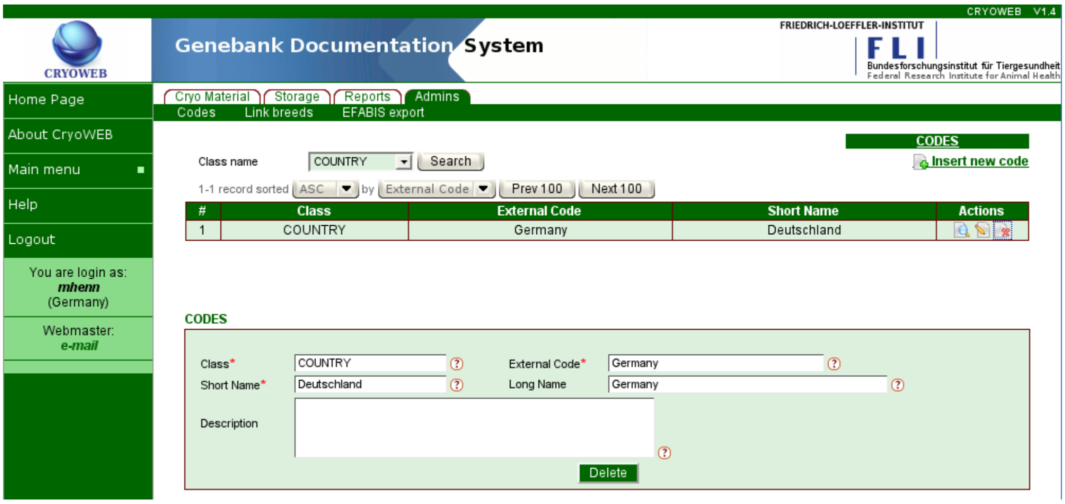
To delete a country name it must not be used, i.e. there cannot be any contacts from this country registered in the database. Therefore, before deleting a country name, you must delete all contacts from this country (if that is what you want to do).

If the country name is not used, click on **Admins**▷**Codes**. From the drop-down list **Class name** choose the option **COUNTRY** and click the **Search** button. In the list below find the line containing the country name and click the **Delete** (right) icon in the **Actions** section of this line. The data for this country will be shown in the **Codes** form below.

To erase the country, click on the **Delete** button in the bottom of the form (Figure 8.24). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**.



You are login as:
mhenn
(Germany)

Webmaster:
e-mail

Class name: COUNTRY

1-1 record sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	COUNTRY	Germany	Deutschland	

CODES

Class*: COUNTRY
External Code*: Germany
Short Name*: Deutschland
Long Name: Germany
Description:

Figure 8.24: Deleting the country name "Germany"

8.6 Material types list management

In this section you will learn how to add, correct and remove material type (semen, embryos, etc.) from the list used on the **Protocols** form and on the forms in the **Reports** tab.

8.6.1 Adding a new material type

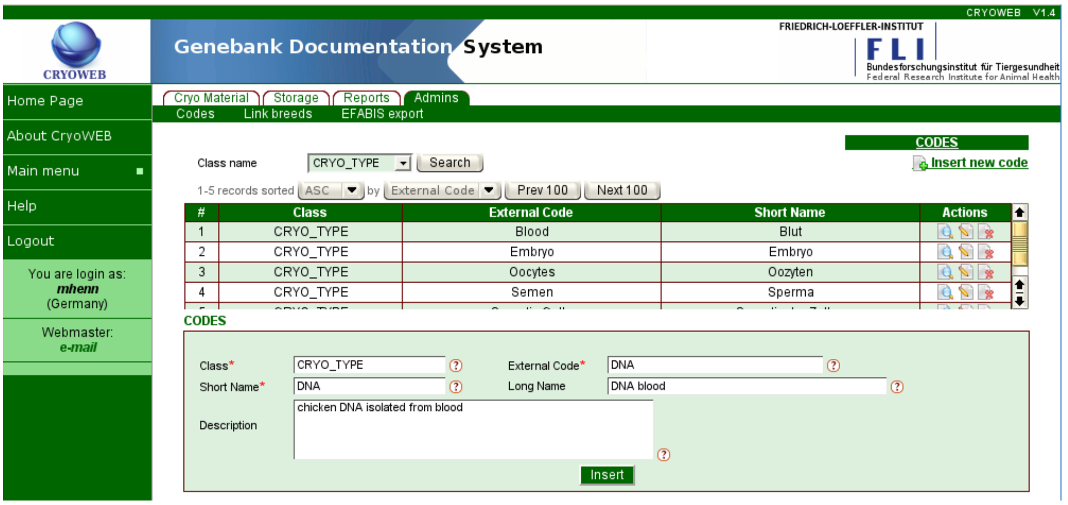
To add a new materialtype, click on **Admins**▷**Codes**. From the drop-down list **Class name** choose the option **CRYO_TYPE** and click the **Search** button.

If there are any material types registered in the database, they will be listed below. Check if the the new type is not already in the database.

If the material type is not in the database, click on the **Insert new code** to start filling the data for it. In the **Codes** form below the list, the system will fill for you automatically the class as **CRYO_TYPE**, and this value cannot be changed.

Enter in the **External Code** field the English name of the type. Enter in the **Short Name** field the type name, the way you want to see it in the drop-down lists in CryoWEB, e.g. in your local language, or abbreviated. You must add also long name for this type and, optionally, a description in the respective fields.

To enter the new material type in the database, click the **Insert** button (Figure 8.25). If the insert was successful the new type will be listed above the Codes form.



Class name: CRYO_TYPE

#	Class	External Code	Short Name	Actions
1	CRYO_TYPE	Blood	Blut	
2	CRYO_TYPE	Embryo	Embryo	
3	CRYO_TYPE	Oocytes	Oozyten	
4	CRYO_TYPE	Semen	Sperma	

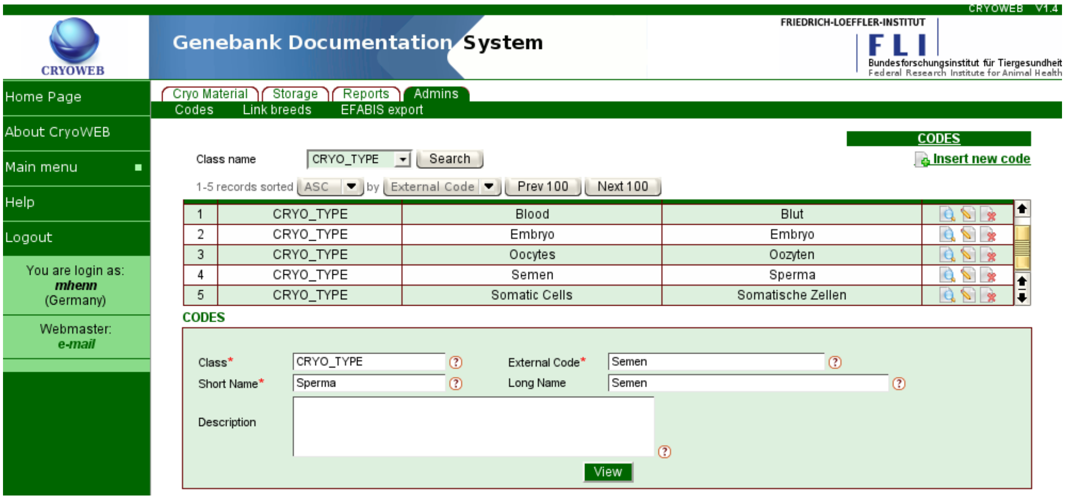
Class*: CRYO_TYPE
External Code*: DNA
Short Name*: DNA
Long Name: DNA blood
Description: chicken DNA isolated from blood

Figure 8.25: Adding a new material type - “DNA”

8.6.2 Viewing material type data

Open **Admins**▷**Codes**. From the drop-down list **Class name** choose the option **CRYO_TYPE**, and click the **Search** button.

The list of all material types registered in the database is shown in the search results table in groups of 100. These summaries include the **External Code** and the **Short Name** of the type.



1	CRYO_TYPE	Blood	Blut
2	CRYO_TYPE	Embryo	Embryo
3	CRYO_TYPE	Oocytes	Oozyten
4	CRYO_TYPE	Semen	Sperma
5	CRYO_TYPE	Somatic Cells	Somatische Zellen

Class* CRYO_TYPE
External Code* Semen
Short Name* Sperma
Long Name Semen
Description

Figure 8.26: View material type data

To view the complete data for a certain type, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the material type name you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the material type will be shown in the **Codes** form below (Figure 8.26).

8.6.3 Correcting material type data

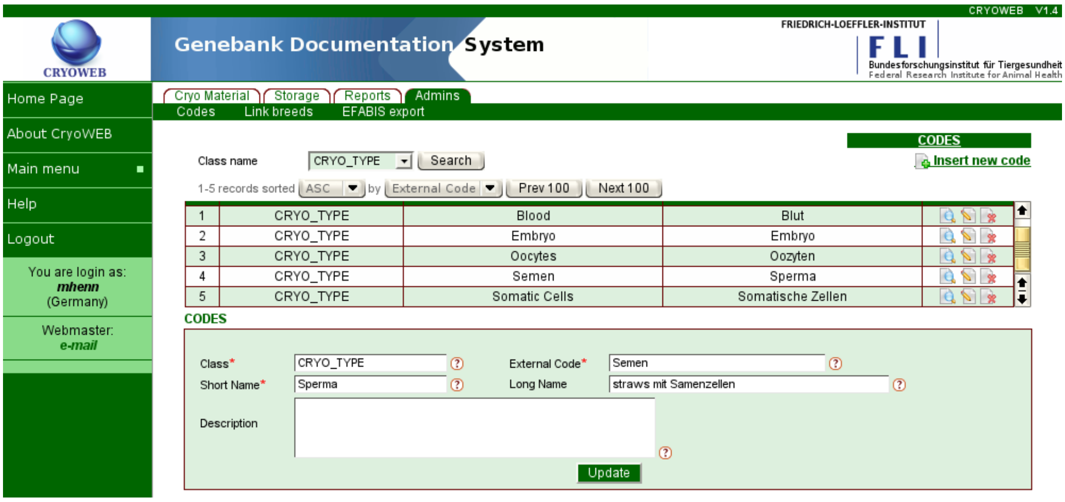
To correct a material type data, click on **Admins** ▷ **Codes**.

From the drop-down list **Class** choose the option **CRYO_TYPE**, and click the **Search** button.

In the list below find the line containing the material type name, and click the **Update** (middle) icon in the **Actions** section of this line. The data for the type will be shown in the **Codes** form below.

Make your corrections in the respective form fields, and click the **Update** button in the bottom of the form to submit the changes to the database (Figure 8.27).

To check that the changes were successfully submitted, find the line in the list containing the material type, and click the **View** (left) icon in the **Actions** section of that line. The data in the **Codes** form will be re-read from the database.



Class name: CRYO_TYPE

1-5 records sorted ASC by External Code

1	CRYO_TYPE	Blood	Blut
2	CRYO_TYPE	Embryo	Embryo
3	CRYO_TYPE	Oocytes	Oozyten
4	CRYO_TYPE	Semen	Sperma
5	CRYO_TYPE	Somatic Cells	Somatische Zellen

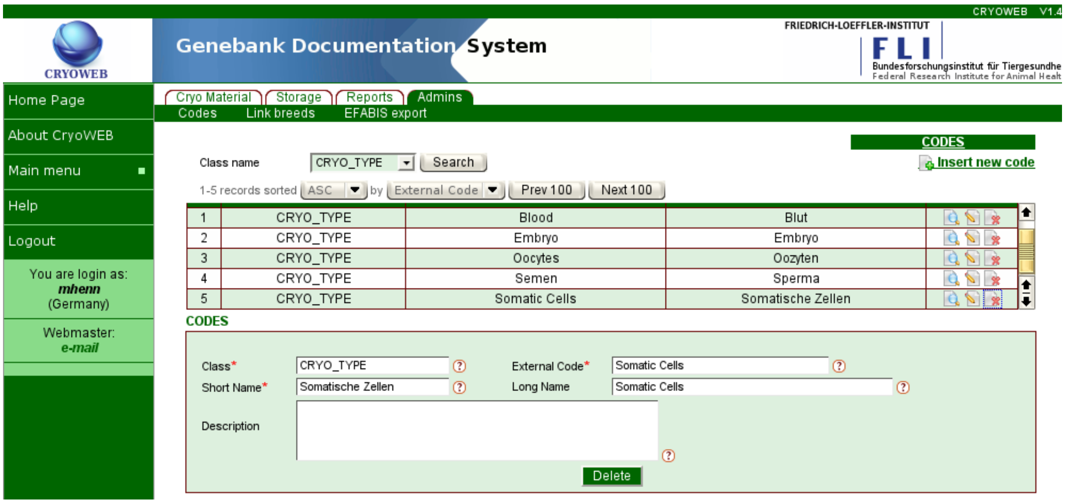
CODES

Class* CRYO_TYPE
External Code* Semen
Short Name* Sperma
Long Name straws mit Samenzellen
Description

Figure 8.27: Correcting a material type data

8.6.4 Deleting a material type

To delete a material type it must not be used, i.e. there should be no protocols for this type registered in the database. Therefore, before deleting a material type, you must delete all protocols from this type (if this is what you want to do).



Class name: CRYO_TYPE

1-5 records sorted ASC by External Code

1	CRYO_TYPE	Blood	Blut
2	CRYO_TYPE	Embryo	Embryo
3	CRYO_TYPE	Oocytes	Oozyten
4	CRYO_TYPE	Semen	Sperma
5	CRYO_TYPE	Somatic Cells	Somatische Zellen

CODES

Class* CRYO_TYPE
External Code* Somatic Cells
Short Name* Somatische Zellen
Long Name Somatic Cells
Description

Figure 8.28: Deleting the material type “Somatic Cells”

If the type is not used, click on **Admins**▷**Codes**. From the drop-down list **Class name** choose the option **CRYO_TYPE** and click the **Search** button. In the list below find the line containing the material type and click the **Delete** (right) icon in the **Actions** section of this line. The data for this type will be shown in the **Codes** form below.

To erase the type, click on the **Delete** button in the bottom of the form (Figure 8.28). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

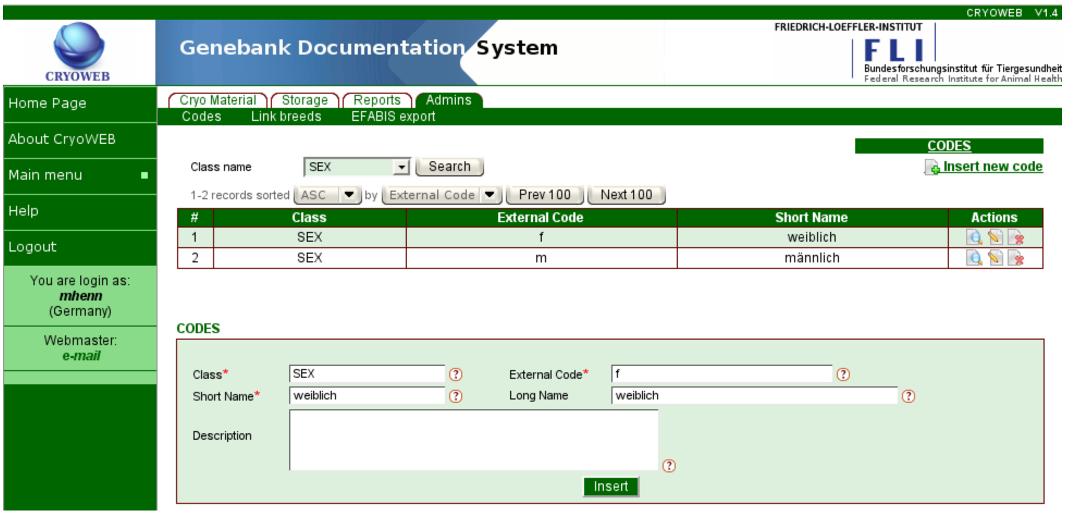
will be shown. Confirm with **OK**.

8.7 Management of sex codes

In this section you will learn how to add, correct and remove codes from the sex list used on the **Animals** form.

8.7.1 Adding a new sex code

To add a new code for a gendertype, click on **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **SEX** and click the **Search** button.



You are login as: *mhenn* (Germany)

Webmaster: *e-mail*

Class name: SEX

1-2 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	SEX	f	weiblich	
2	SEX	m	männlich	

CODES

Class*: SEX
External Code*: f
Short Name*: weiblich
Long Name: weiblich
Description:

Figure 8.29: Adding a new sex code - “weiblich”

If there are any codes for sex registered in the database, they will be listed below. Check if the the new code is not already in the database.

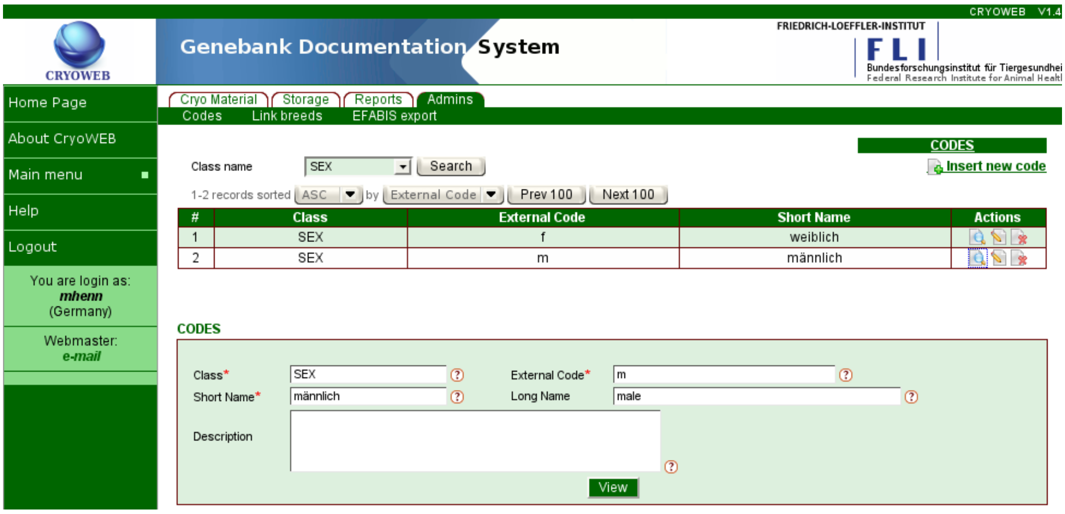
If the sex is not in the database, click on the **Insert new code** to start filling the data for it. In the **Codes** form below the list, the system will fill for you automatically the class as **SEX**, and this value cannot be changed.

Enter in the **External Code** field the English name of the sex. Enter in the **Short Name** field the sex name, the way you want to see it in the drop-down lists in CryoWEB, e.g. in your local language, or abbreviated. You must add also long name for this sex and, optionally, a description in the respective fields.

To enter the new sex code in the database, click the **Insert** button (Figure 8.29). If the insert was successful the new code will be listed above the **Codes** form.

8.7.2 Viewing sex code data

Open **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **SEX**, and click the **Search** button.



Class name: SEX

1-2 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	SEX	f	weiblich	
2	SEX	m	männlich	

CODES

Class*: SEX

External Code*: m

Short Name*: männlich

Long Name: male

Description:

Figure 8.30: View sex code data

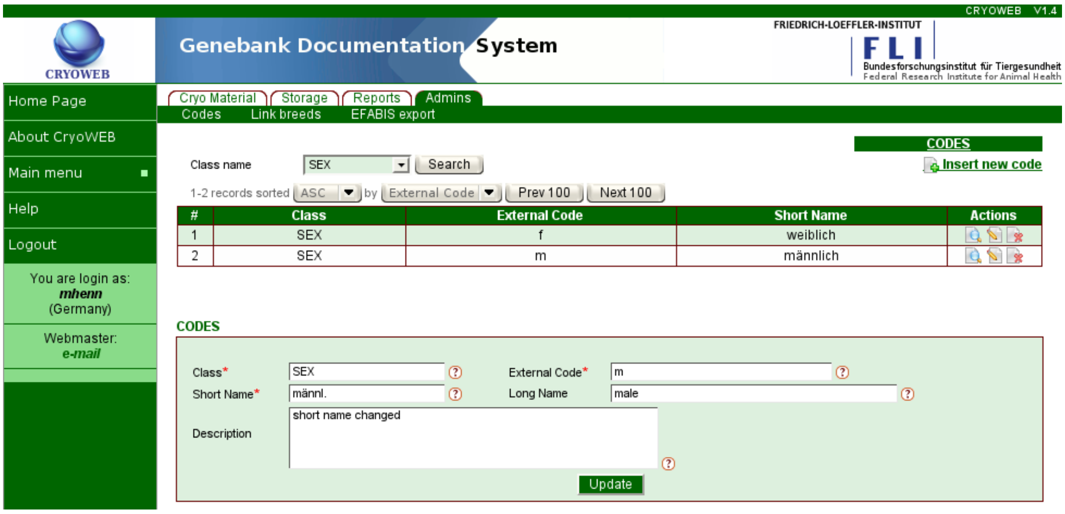
The list of all codes for sex registered in the database is shown in the search results table. These summaries include the **External Code** and the **Short Name** of the code.

To view the complete data for a certain gender, navigate through the table until you find the row containing the code you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the sex code will be shown in the **Codes** form below (Figure 8.30).

8.7.3 Correcting sex code data

To correct a sex code data, click on **Admins** ▷ **Codes**.



You are login as: **mhenn** (Germany)

Class name: SEX

1-2 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	SEX	f	weiblich	
2	SEX	m	männlich	

CODES

Class*: SEX

External Code*: m

Short Name*: männl.

Long Name: male

Description: short name changed

Figure 8.31: Correcting a sex code data

From the drop-down list **Class** choose the option **SEX**, and click the **Search** button. In the list below find the line containing the gender code, and click the **Update** (middle) icon in the **Actions** section of this line. The data for the type will be shown in the **Codes** form below.

Make your corrections in the respective form fields, and click the **Update** button in the bottom of the form to submit the changes to the database (Figure 8.31).

To check that the changes were successfully submitted, find the line in the list containing the sex code, and click the **View** (left) icon in the **Actions** section of that line. The data in the **Codes** form will be re-read from the database.

8.7.4 Deleting a sex code

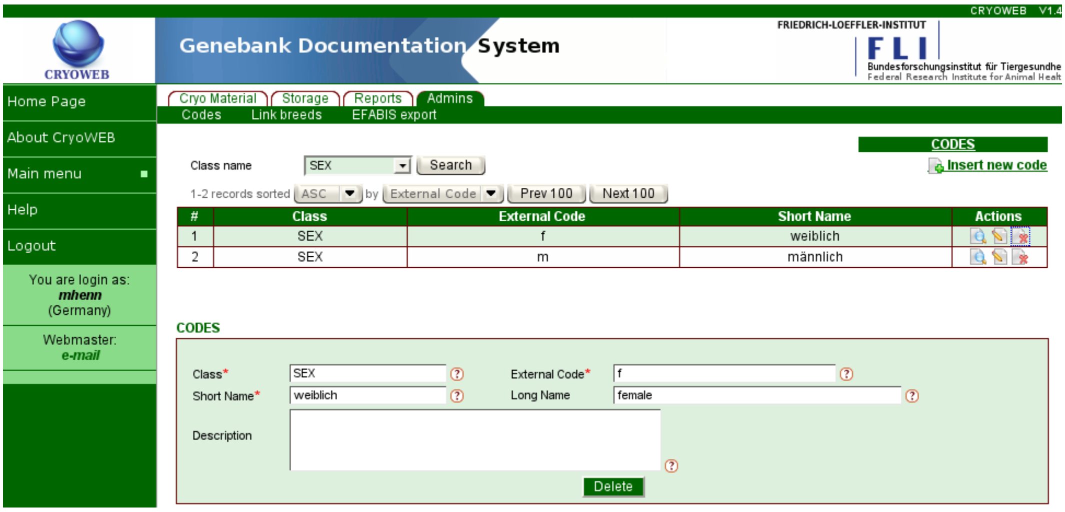
To delete a sex code it must not be used, i.e. there must not be any animals from this gender registered in the database. Therefore, before deleting a sex code, you must delete all animals from this gender (if this is what you really want to do).

If the code is not used, click on **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **SEX** and click the **Search** button. In the list below find the line containing the code and click the **Delete** (right) icon in the **Actions** section of this line. The data for this gender will be shown in the **Codes** form below.

To erase the gender, click on the **Delete** button in the bottom of the form (Figure 8.32). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**.



Class name SEX

1-2 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	SEX	f	weiblich	
2	SEX	m	männlich	

Class* SEX

External Code* f

Short Name* weiblich

Long Name female

Description

Figure 8.32: Deleting the sex code “weiblich”

8.8 Mime types list management

CryoWEB comes with predefined list of mime types (a two-part identifier for file formats). This list allows the browser to display or output the files you have uploaded in CryoWEB. In this section you will learn how to add, correct and remove a mime type in CryoWEB.

8.8.1 Adding new mime type

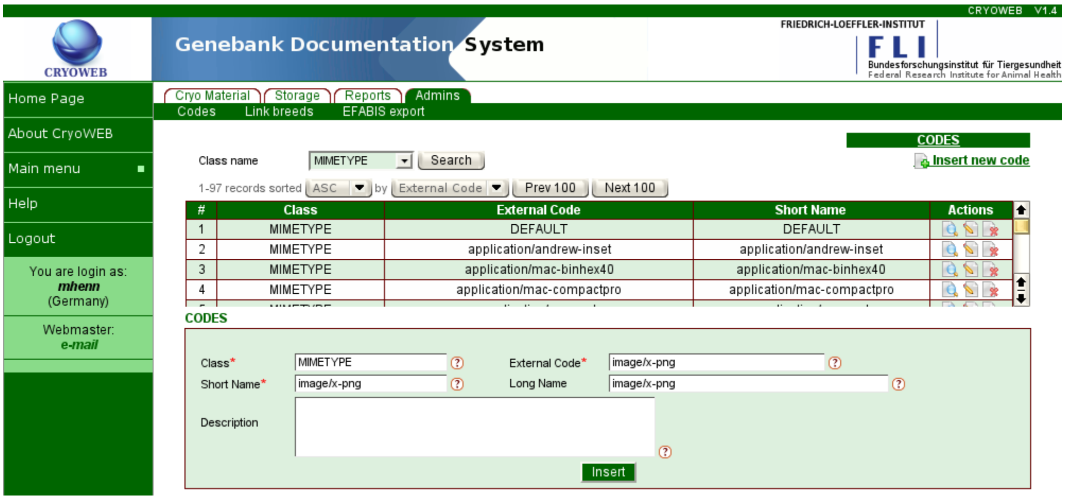
To add a new mimetype, click on **Admins** ▷ **Codes**. From the drop-down list **Class name** choose the option **MIMETYPE** and click the **Search** button.

The mime types registered in the database will be listed below. Check if the the new type is not already in the database.

If the mime type is not in the database, click on the **Insert new code** to start filling in the data for it. In the **Codes** form below the list, the system will fill for you automatically the class as **MIMETYPE**, and this value cannot be changed.

Enter in the **External Code**, **Short Name**, and **Long Name** fields the mime type (same in the three fields) and fill a description in the respective field.

To enter the new mime type in the database, click the **Insert** button (Figure 8.33). If the insert was successful the new type will be listed above the **Codes** form.



Class name: MIMETYPE

1-97 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
1	MIMETYPE	DEFAULT	DEFAULT	
2	MIMETYPE	application/andrew-inset	application/andrew-inset	
3	MIMETYPE	application/mac-binhex40	application/mac-binhex40	
4	MIMETYPE	application/mac-compactpro	application/mac-compactpro	

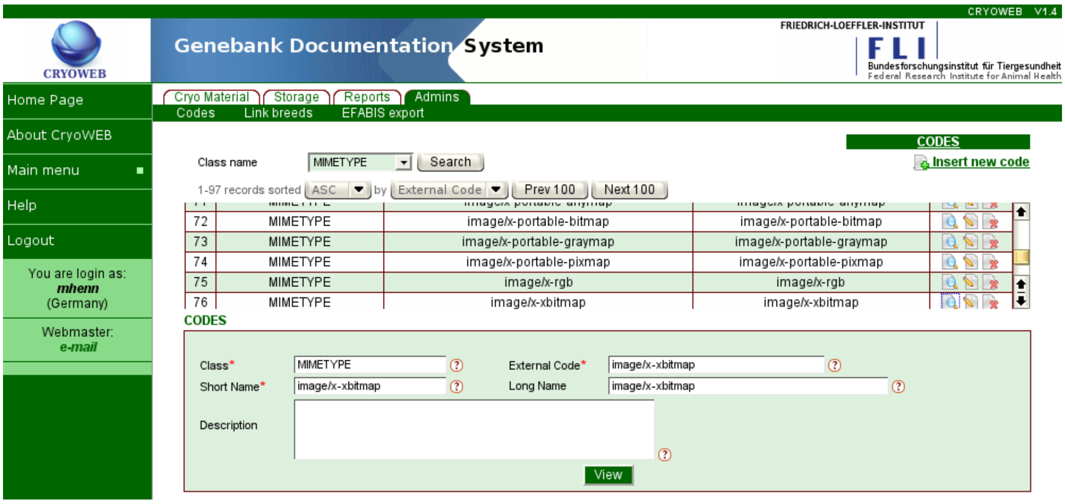
CODES

Class*: MIMETYPE
External Code*: image/x-png
Short Name*: image/x-png
Long Name: image/x-png
Description:

Figure 8.33: Adding a new mime type - “image/x-png”

8.8.2 Viewing mime type data

Open **Admins ▷ Codes**. From the drop-down list **Class name** choose the option **MIMETYPE**, and click the **Search** button.



Class name: MIMETYPE

1-97 records sorted ASC by External Code

#	Class	External Code	Short Name	Actions
72	MIMETYPE	image/x-portable-bitmap	image/x-portable-bitmap	
73	MIMETYPE	image/x-portable-graymap	image/x-portable-graymap	
74	MIMETYPE	image/x-portable-pixmap	image/x-portable-pixmap	
75	MIMETYPE	image/x-rgb	image/x-rgb	
76	MIMETYPE	image/x-xbitmap	image/x-xbitmap	

CODES

Class*: MIMETYPE
External Code*: image/x-xbitmap
Short Name*: image/x-xbitmap
Long Name: image/x-xbitmap
Description:

Figure 8.34: View mime type data

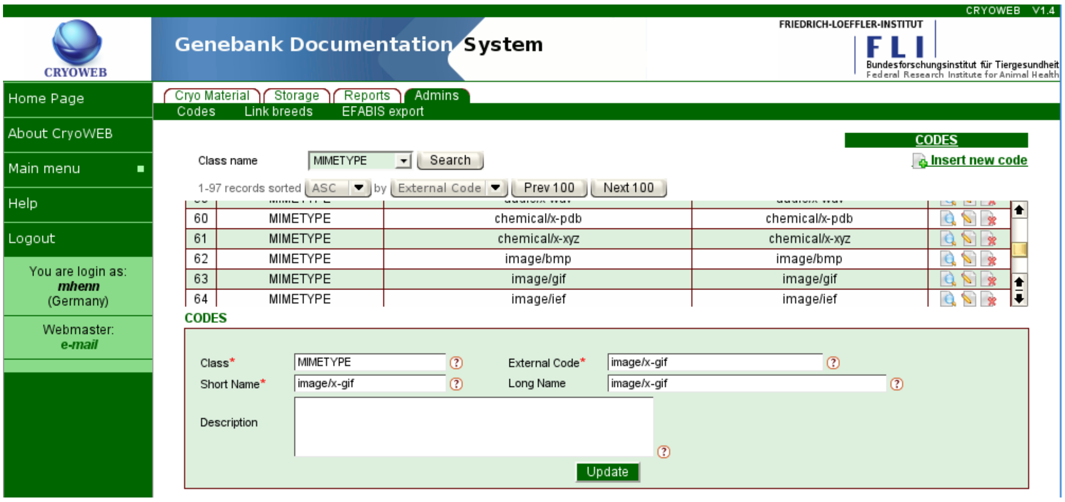
The list of all mime types registered in the database is shown in the search results table in groups of 100. These summaries include the **External Code** and the **Short Name** of the type.

To view the complete data for a certain mime type, navigate through the table (by scrolling the groups with the buttons **Prev 100**, **Next 100** and scrolling the table itself) until you find the row containing the mime type name you are looking for.

Then click on the View (left) icon in the **Actions** section of this line. The submit button label should change to **View**. The data for the mime type will be shown in the **Codes** form below (Figure 8.34).

8.8.3 Correcting mime type data

To correct a mime type data, click on **Admins**▷**Codes**.



Class name: MIMETYPE

1-97 records sorted ASC by External Code

60	MIMETYPE	chemical/x-pdb	chemical/x-pdb
61	MIMETYPE	chemical/x-xyz	chemical/x-xyz
62	MIMETYPE	image/bmp	image/bmp
63	MIMETYPE	image/gif	image/gif
64	MIMETYPE	image/ief	image/ief

Class*: MIMETYPE

External Code*: image/x-gif

Short Name*: image/x-gif

Long Name: image/x-gif

Description:

Figure 8.35: Correcting a mime type data

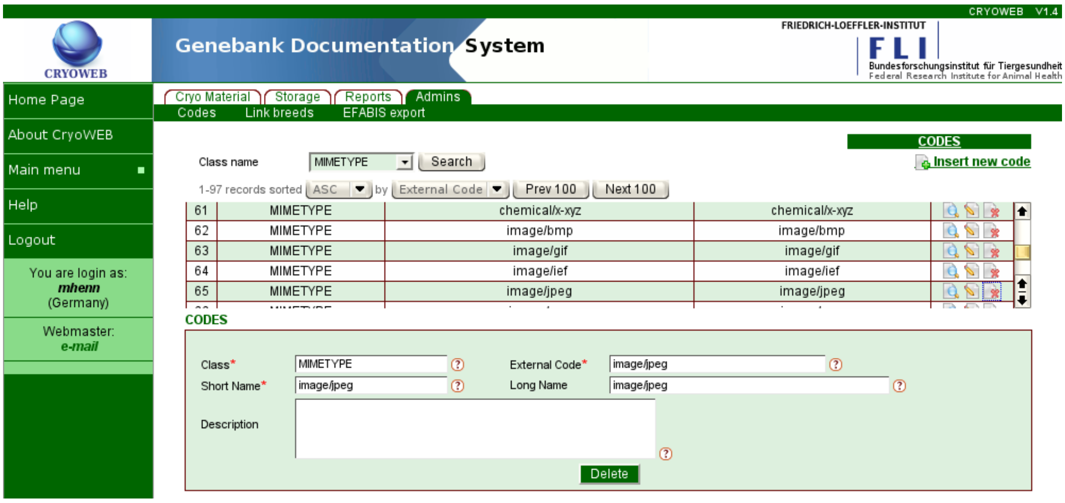
From the drop-down list **Class** choose the option **MIMETYPE**, and click the **Search** button. In the list below find the line containing the mime type name, and click the **Update** (middle) icon in the **Actions** section of this line. The data for the type will be shown in the **Codes** form below.

Make your corrections in the respective form fields, and click the **Update** button in the bottom of the form to submit the changes to the database (Figure 8.35).

To check that the changes were successfully submitted, find the line in the list containing the mime type, and click the **View** (left) icon in the **Actions** section of that line. The data in the **Codes** form will be re-read from the database.

8.8.4 Deleting a mime type

To delete a mime type it must not be used, i.e. there should be no files of this type uploaded in the database. Therefore, before deleting a mime type, you must delete all files of this type (if this is really what you want to do).



You are login as:
mhenn
(Germany)

Class name: MIMETYPE

1-97 records sorted ASC by External Code

61	MIMETYPE	chemical/x-xyz	chemical/x-xyz
62	MIMETYPE	image/bmp	image/bmp
63	MIMETYPE	image/gif	image/gif
64	MIMETYPE	image/ief	image/ief
65	MIMETYPE	image/jpeg	image/jpeg

Class*: MIMETYPE
External Code*: image/jpeg
Short Name*: image/jpeg
Long Name: image/jpeg
Description:

Figure 8.36: Deleting the mime type “image/jpeg”

If the type is not used, click on **Admins ▷ Codes**. From the drop-down list **Class name** choose the option **MIMETYPE** and click the **Search** button. In the list below find the line containing the mime type and click the **Delete** (right) icon in the **Actions** section of this line. The data for this type will be shown in the **Codes** form below. To erase the type, click on the **Delete** button in the bottom of the form (Figure 8.36). A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown. Confirm with **OK**.

8.9 User management

The user management is done via the **Access Rights Manager** (**ARM**) web page, which should be installed together with CryoWEB and, in fact, is part of the default appliance. For all tasks in that group you should be logged in the ARM with the administrator account. There are 4 types of user accounts - **reader**, **operator**, **manager** and **administrator**. The **reader** has read-only access to the common forms and data and no access to the administrative part. The **operator** has reader rights and access to add, modify and erase common data. The **manager** has, in addition to the operator privileges, full access to the administrative part. The **administrator** has privileges for user management.

8.9.1 Logging in to the ARM

Open the ARM web page in your browser. By default, the URL of the ARM page is the URL of the CryoWEB page, with http replaced by https. On the left side of the screen (Figure 8.37) choose English from the Language drop-down list, then from the Project drop-down list choose dagenbank for the project name. Fill your user name and password (provided to you by the administrator) and click the **Log-in** button to enter the ARM page.

Language: English

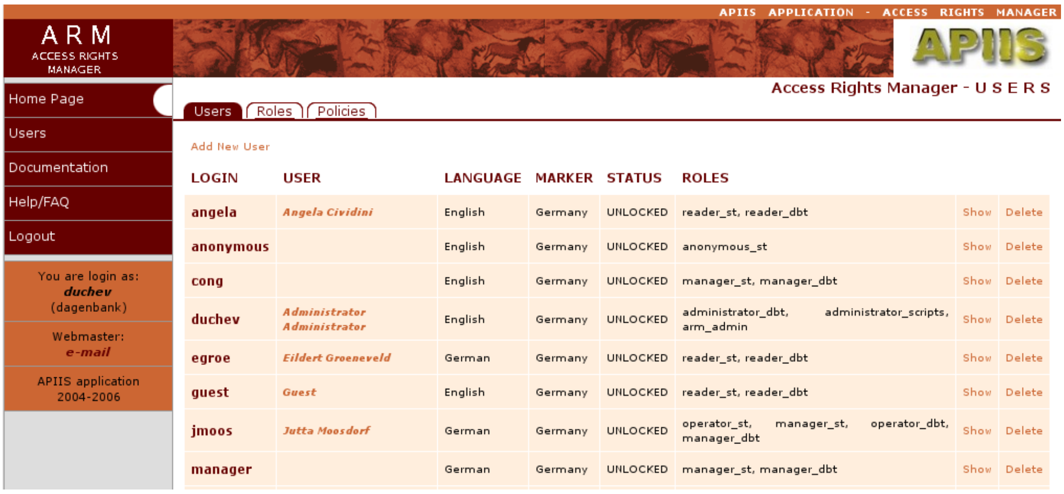
Project: dagenbank

User name: duchev

Password: ••••

Figure 8.37: Log into Access Rights Manager

If the login was successful, you will see the list of users registered in CryoWEB (Figure 8.38).



Access Rights Manager - U S E R S

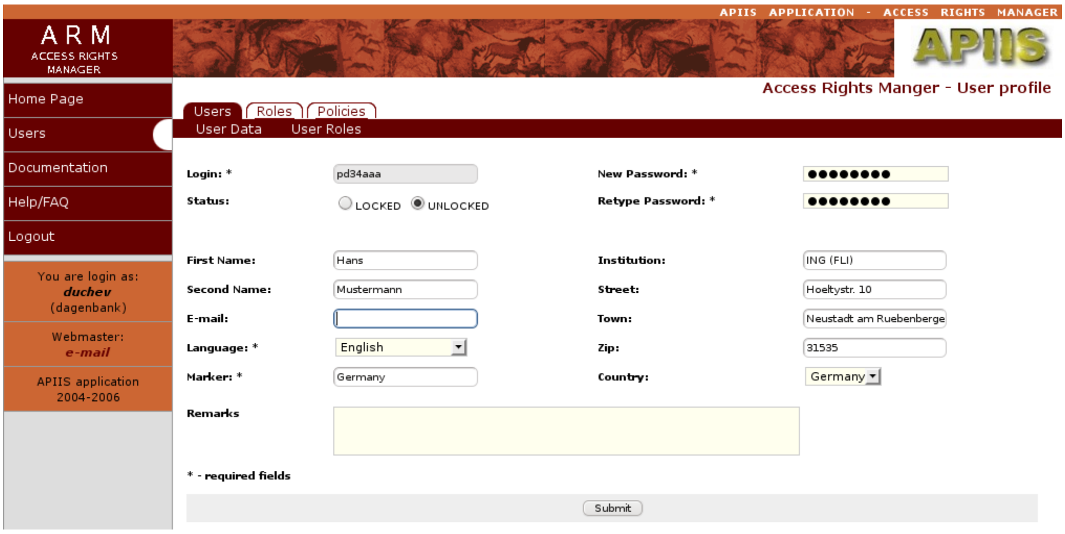
Add New User

LOGIN	USER	LANGUAGE	MARKER	STATUS	ROLES		
angela	*Angela Cividini*	English	Germany	UNLOCKED	reader_st, reader_dbt	Show	Delete
anonymous		English	Germany	UNLOCKED	anonymous_st	Show	Delete
cong		English	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete
duchev	*Administrator Administrator*	English	Germany	UNLOCKED	administrator_dbt, administrator_scripts, arm_admin	Show	Delete
egroe	*Eildert Groeneveld*	German	Germany	UNLOCKED	reader_st, reader_dbt	Show	Delete
guest	*Guest*	English	Germany	UNLOCKED	reader_st, reader_dbt	Show	Delete
jmoos	*Jutta Moosdorf*	German	Germany	UNLOCKED	operator_st, manager_st, operator_dbt, manager_dbt	Show	Delete
manager		German	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete

Figure 8.38: List of users registered in a CryoWEB system

8.9.2 Adding a new user

To add a new user click on the **Users** tab. Then click the **Add new user** link below.



Access Rights Manger - User profile

Login: * pd34aaa

Status: ○ LOCKED ● UNLOCKED

New Password: * ●●●●●●●●

Retype Password: * ●●●●●●●●

First Name: Hans

Second Name: Mustermann

E-mail:

Language: * English

Marker: * Germany

Institution: ING (FLI)

Street: Hoeltystr. 10

Town: Neustadt am Ruebenberge

Zip: 31535

Country: Germany

Remarks

*** - required fields**

Figure 8.39: Creating a new user pd34aaa

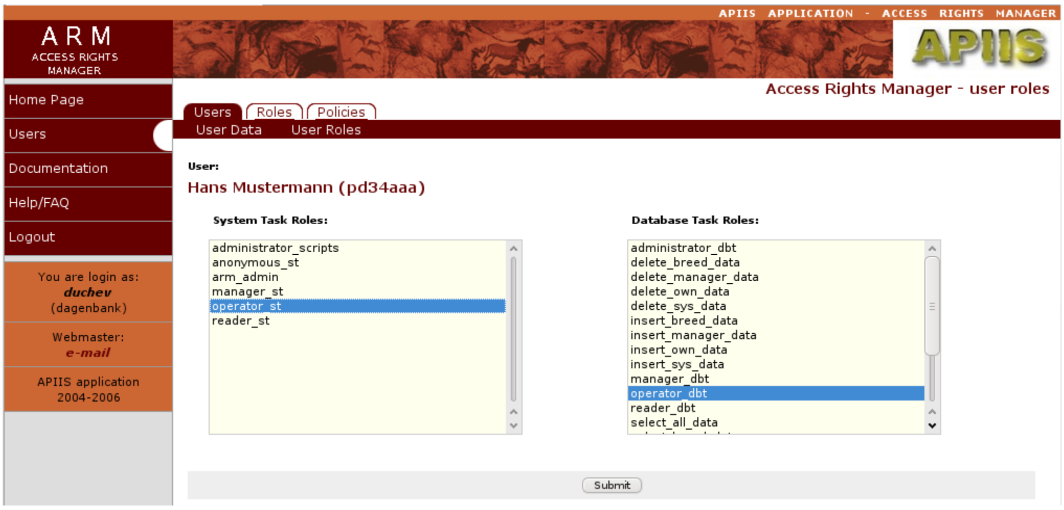
Fill in the **Login** field with the user name. It should contain only English letters and numbers, starting with letter. The name must not contain any special characters or upper case. Then fill in the password in the **New Password** field and repeat it in the **Retype Password** field below. Make sure the **UNLOCKED** radio button for the **Status** is checked. From the **Language** drop-down list choose English.

If you use a standard CryoWEB software and have not made additional setting for various user markers, the **Marker** field will be automatically filled by the system with a default value and you must not change it. If you have a special setup with various markers, type in the **Marker** field type the respective user marker.

Fill in the user names and contact details in the other fields and submit the form by clicking the **Submit** button (Figure 8.39). This will create a user account in CryoWEB with the respective login and password.

After the user account is created, you have to assign permissions to this account. Click on the **User Roles** sub-tab, the user name and the login should occur under **User**.

The permissions are grouped in system and database roles which correspond to the 4 accounts types. Choose from the **System Task Roles** list the value for the desired account, e.g. **operator_st** for **operator**. In the same manner choose the database task role from the respective list, e.g. **operator_dbt** for **operator**. To add the permissions, click the **Submit** button (Figure 8.40).



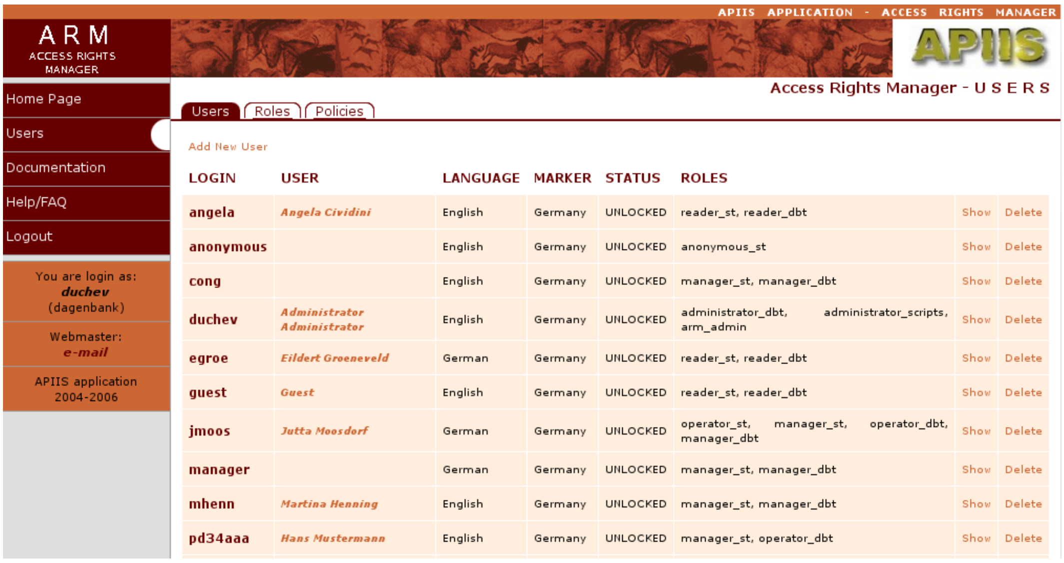
User:
Hans Mustermann (pd34aaa)

System Task Roles: operator_st

Database Task Roles: operator_dbt

Figure 8.40: Adding operator role to user pd34aaa

To check if the operation was successful click on the **Users** tab, find the line for the new user and check the data as shown in Figure 8.41.

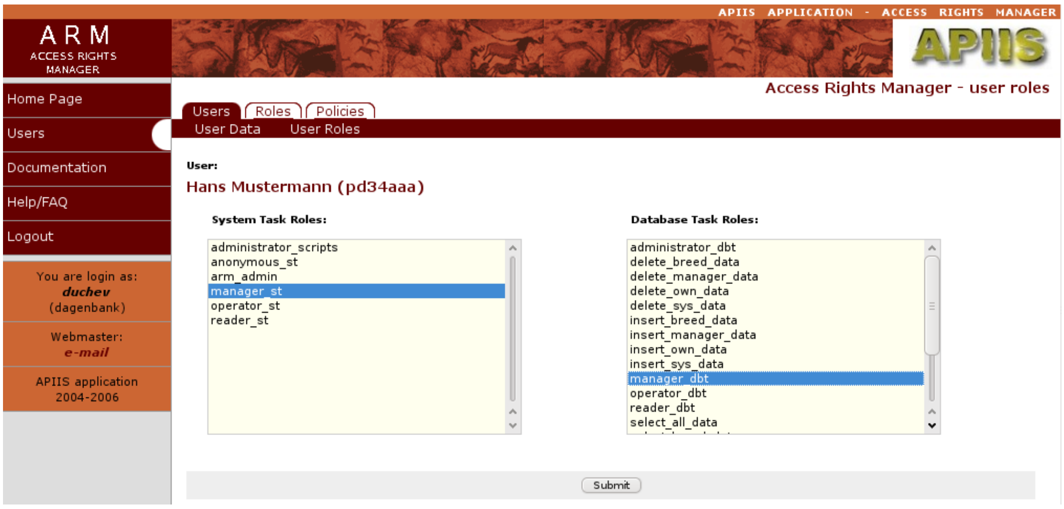


LOGIN	USER	LANGUAGE	MARKER	STATUS	ROLES		
angela	*Angela Cividini*	English	Germany	UNLOCKED	reader_st, reader_dbt	Show	Delete
anonymous		English	Germany	UNLOCKED	anonymous_st	Show	Delete
cong		English	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete
duchev	*Administrator Administrator*	English	Germany	UNLOCKED	administrator_dbt, administrator_scripts, arm_admin	Show	Delete
egroe	*Eildert Groeneveld*	German	Germany	UNLOCKED	reader_st, reader_dbt	Show	Delete
guest	*Guest*	English	Germany	UNLOCKED	reader_st, reader_dbt	Show	Delete
jmoos	*Jutta Moosdorf*	German	Germany	UNLOCKED	operator_st, manager_st, operator_dbt, manager_dbt	Show	Delete
manager		German	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete
mhenn	*Martina Henning*	English	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete
pd34aaa	*Hans Mustermann*	English	Germany	UNLOCKED	manager_st, operator_dbt	Show	Delete

Figure 8.41: The details for the new user pd34aaa listed in the users table

8.9.3 Changing user permissions

To change the user permissions click on the **Users** tab. Find the user login in the list and click on the **Show** link in the line with the user name. The user data is shown in the form. Click on the **User Roles** sub-tab and choose from the **System Task Roles** and **Database Task Roles** lists the new values for the role of the user as shown in Figure 8.42.



User:
Hans Mustermann (pd34aaa)

System Task Roles:

administrator_scripts
anonymous_st
arm_admin
manager_st
operator_st
reader_st

Database Task Roles:

administrator_dbt
delete_breed_data
delete_manager_data
delete_own_data
delete_sys_data
insert_breed_data
insert_manager_data
insert_own_data
insert_sys_data
manager_dbt
operator_dbt
reader_dbt
select_all_data

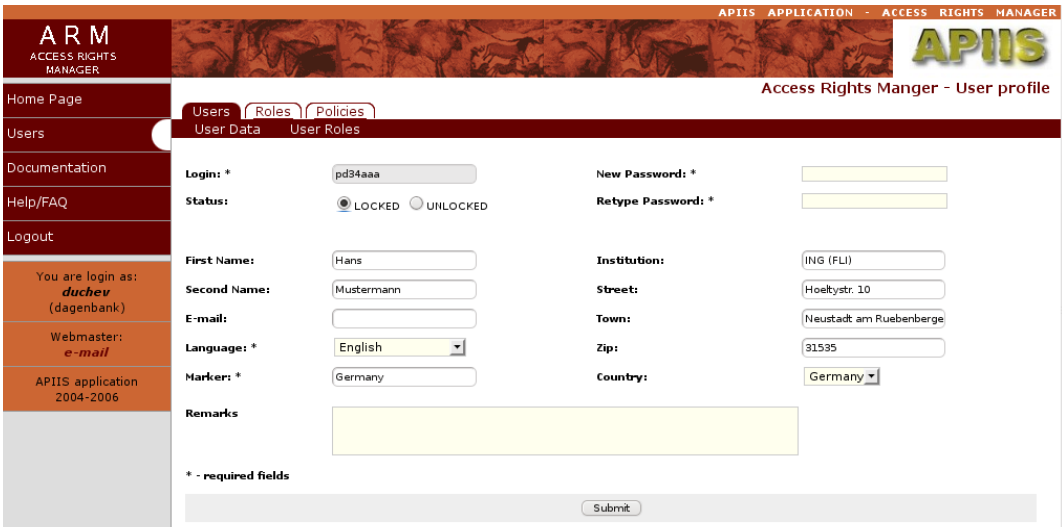
Figure 8.42: Changing user permission for pd34aaa to manager

8.9.4 Blocking and unblocking user account

If a user account is not used anymore it can be deleted or blocked. If an account is deleted then the user name is removed from the system and the related access rights erased. On the other hand the account can be just blocked, then the access data is kept, but the user cannot login in the web page. Later, if the user needs again access, the account must be only unblocked and the user can continue her work as before.

To block the user account, i.e. not allow the user to login in CryoWEB, click on the **Users** tab. Find the user login in the list, and click on the **Show** link in the line with the user name. The user data is shown in the form. Check the **LOCKED** radio button in **Status** and apply the changes by clicking the **Submit** button (Figure 8.43).

To unblock the user account click on the **Users** tab, find the user login in the list and click on the **Show** link in the same line. Check the **UNLOCKED** radio button in **Status** and apply the changes by clicking the **Submit** button.



Login: * pd34aaa

Status: ● LOCKED ○ UNLOCKED

New Password: *

Retype Password: *

First Name: Hans

Second Name: Mustermann

E-mail:

Language: * English

Marker: * Germany

Institution: ING (FLI)

Street: Hoeltystr. 10

Town: Neustadt am Ruebenberge

Zip: 31535

Country: Germany

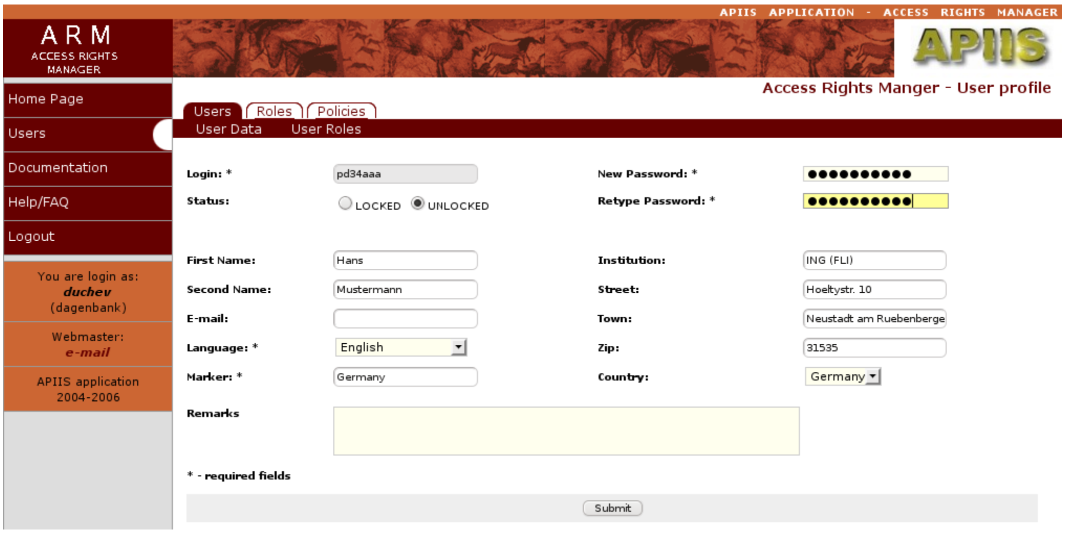
Remarks

* - required fields

Figure 8.43: The user account pd34aaa is now blocked

8.9.5 Changing user password

To change the user password, click on the **Users** tab. Find the user in the list and click on the **Show** link in the line with the user name. The user data is shown in the form. For security reasons, the current password is not shown. Type the new password in the **New Password** and **Retype Password** fields (Figure 8.44). Click the **Submit** button to apply the changes.



You are login as: **duchev** (dagenbank)

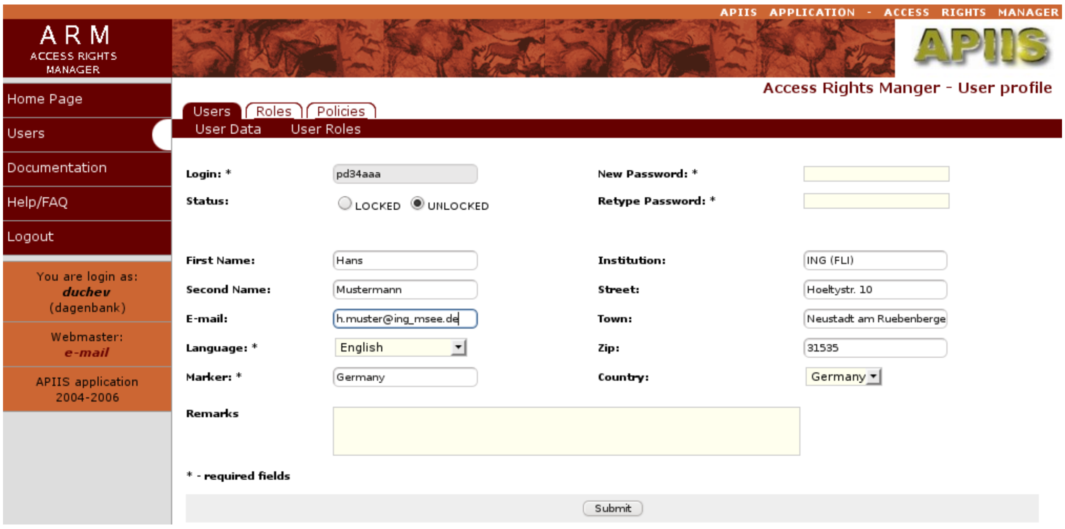
Login: *	pd34aaa	New Password: *	●●●●●●●●●●
Status:	○ LOCKED ● UNLOCKED	Retype Password: *	●●●●●●●●●●
First Name:	Hans	Institution:	ING (FLI)
Second Name:	Mustermann	Street:	Hoeltystr. 10
E-mail:		Town:	Neustadt am Ruebenberge
Language: *	English	Zip:	31535
Marker: *	Germany	Country:	Germany
Remarks			

* - required fields

Figure 8.44: Changing the password for user pd34aaa

8.9.6 Updating user data

To change the user data click on the **Users** tab. Find the user in the list and click on the **Show** link in the line with the user name.



You are login as: **duchev** (dagenbank)

Login: *	pd34aaa	New Password: *	
Status:	○ LOCKED ● UNLOCKED	Retype Password: *	
First Name:	Hans	Institution:	ING (FLI)
Second Name:	Mustermann	Street:	Hoeltystr. 10
E-mail:	h.muster@ing_msee.de	Town:	Neustadt am Ruebenberge
Language: *	English	Zip:	31535
Marker: *	Germany	Country:	Germany
Remarks			

* - required fields

Figure 8.45: Updating the user pd34aaa data - email added

The user data is shown in the form. For security reasons the current password is not shown. Make the corrections in the users data and apply the changes by clicking the **Submit** button (Figure 8.45). Please note that the user login cannot be changed.

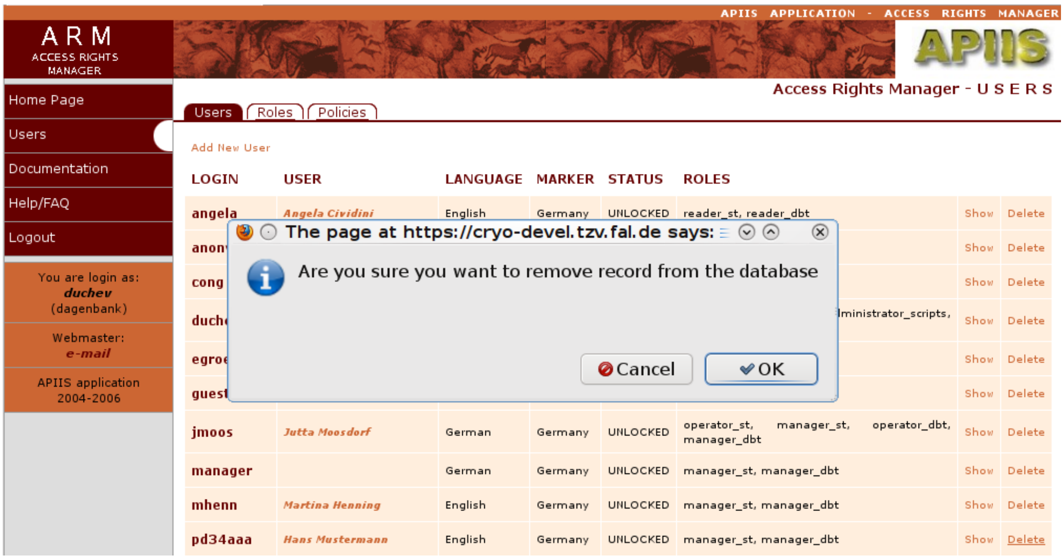
If you want to change the user login, you have to erase this user and create a new one.

8.9.7 Deleting user

To erase the user click on the **Users** tab. Find the user in the list and click on the **Delete** link in the line with the user name. A confirmation dialog

```
Are you sure you want to remove record from the database?
```

will be shown as in Figure 8.46. Confirm with **OK**.



The page at https://cryo-devel.tzv.fal.de says:

Are you sure you want to remove record from the database

LOGIN	USER	LANGUAGE	MARKER	STATUS	ROLES		
angela	Angela Cividini	English	Germany	UNLOCKED	reader_st, reader_dbt	Show	Delete
anon						Show	Delete
cong						Show	Delete
duch					lministrator_scripts,	Show	Delete
egroe						Show	Delete
guest						Show	Delete
jmoos	Jutta Moosdorf	German	Germany	UNLOCKED	operator_st, manager_st, operator_dbt, manager_dbt	Show	Delete
manager		German	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete
mhenn	Martina Henning	English	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete
pd34aaa	Hans Mustermann	English	Germany	UNLOCKED	manager_st, manager_dbt	Show	Delete

Figure 8.46: Deleting the user pd34aaa

9 Error messages

In this chapter we list the main error messages, along with their meaning and their common causes. Usually, the field in question will be marked in red on the form.

```
<field name>:Value must not be NULL
The passed value was: undefined
```

This error message is shown when you try to insert, or update a record, but one of the mandatory fields is left empty. Fill the field and resubmit the form.

```
<field name>:Wrong date format
Only 4 digit years are allowed (<part of date>)
```

The year part of a date field is not four digit, e.g. you have typed 09 instead of 2009 (23-11-09 should be 23-11-2009). Correct the date and resubmit the form.

```
<field name>:Not a valid date
```

The data entered in a date field do not represent a valid date, e.g. 23-13-2008 was entered. Correct the date and resubmit the form.

```
<field name>:Wrong date format
Could not split date into 3 parts
```

A date field is not filled following the dd-mm-yyyy format, e.g. instead of 11-04-2009, 11.04-2009 was entered.

```
loc_<number>_5:Please enter at least one location
```

The **Unit** cell field, which is mandatory, was left empty. Enter the identification of the cell (the lowest location hierarchy level) in this field and resubmit the form.

```
loc_<number>_4_loop:Missing data
```

The **Compartment** field, which is mandatory, was left empty. Choose the compartment from the drop-down list (you must first choose the **Storage**, **Tank** and **Canister** from the respective lists).

```
db_animal_loop:The semen donor is not a male animal.
```

The animal identification chosen as a donor on the Sample form belongs to a female animal, but the sample protocol is for semen. If the sample is of material type semen, choose the right animal id. If the sample type is not semen, choose the correct protocol from the **Protocol name** drop-down list.

```
production_dt:Data error in CHECK rule
Data "<date1>" is not  "<= <date2> freezing_dt"
```

The date entered in the production date field follows chronologically after the freezing date. The production date should always be before or the same as the freezing date.

```
freezing_dt:Data error in CHECK rule
Data "<date1>" is not  ">= <date2> production_dt"
```

This error message is shown when the date entered in the production date field follows chronologically the freezing date. The production date should always be earlier than the freezing date.

```
production_dt:Data error in CHECK rule
The production/freezing date "<date1>" is after
the insert/moving date "<date2>"
```

This error message is shown when on sample update the production date is changed to a date which follows chronologically the sample entry date. The production date should always be before or the same as the entry date.

```
freezing_dt:Data error in CHECK rule
The production/freezing date "<date1>" is after
the insert/moving date "<date2>"
```

This error message is shown when on sample update the freezing date is changed to a date which follows chronologically the sample entry date. The freezing date should always be before or the same as the entry date.

```
loc_<number>_entry_dt:Data error in CHECK rule
The date "<date1>" is not  ">=  <date2> (production_dt)"
```

This error message is shown when the date entered in the entry date field -follows chronologically the freezing date. The entry date in the storage should always be after or the same as the production date.

```
loc_<number>_entry_dt:Data error in CHECK rule
The date "<date1>" is not  ">= <date2> (freezing_dt)"
```

This error message is shown when the date entered in the entry date field for the location follows chronologically before the freezing date. The entry date in storage should always be after or the same as the freezing date.

```
<field name>:Must be a number
```

The data entered in the field are not numeric, but numeric data are expected.

```
<field name>:Data error in CHECK rule
Data "<value>" is not  ">= 0"
```

The data expected in that field must be a non-negative number.

```
<field name>:Empty date
```

This date field is mandatory, but no value was entered by the user.

```
Parameter missing: password
```

This error message is shown if the user did not enter the password during log in.

```
Authentication failed
```

This error message is shown if the user name and password are not registered in the system. Contact the CryoWEB administrator to check again your login credentials.

```
There are already vessel units in this location. Update the
    existing record instead inserting new one
```

This error message is shown when you try to insert a new sample distribution record, but in this location there are already units from the same sample.

```
There are already vessel units in this location. Delete this record
     and update the other
```

This error message is shown when you try to correct the location of sample distribution record but the new location already contains units from the same sample.

```
There are already vessel units with different status in this
    location
```

This error message is shown when you try to move part of the sample to a location where there are already units from the same sample, but with different status. The system rule is that in one cell all the units from one sample must have the same status.

```
The old and new status are the same
```

This error message is shown when you try to change the status of part of the sample, but have entered the same status.

```
Cannot change the availability status on this date! There is later
    movement/status change from this location
```

This error message is shown when you try to change the status of part of the sample, but some units have been moved from/to this part to/from other locations.

```
Cannot revert the action! There is later movement/status change
    from this location
```

This error message is shown when you try to revert a movement or status change, but this was not the last action in this location. You can revert only the chronologically last action.

```
There is already movement from/to this location. Cannot update the
    record
```

This error message is shown when you try to correct a sample distribution record, but there was already a movement from or to this location. If you want to correct the record, you have first to revert all movements records.

```
There is already movement from/to this location. Cannot delete the
    record
```

This error message is shown when you try to delete a sample distribution record, but there was already a movement from or to this location. In this case you have first to revert all movements records.

```
This record is referenced by another record.
Please delete first all the referencing records.
```

This error message is shown when you try to delete data that is used (referenced) from other records. For example: if this error message occurs during deletion of tank, canister, etc. it shows that the storage you try to delete is not empty, i.e. there are still samples stored in it.

```
Cannot move the storage to this level
```

This error message is shown when you try to move an element of the storage hierarchy to a wrong level, e.g. trying to move tank into canister.

```
There is already a container with the same label in the target
    location
```

This error message is shown when you try to move via the **Move Containers** form a container to a destination which already contains container with the same name. For example, let there are 2 storage buildings - B1 and B2 and in each building there is a tank T1. If you try to move the T1 tank from B1 to B2 CryoWEB will raise the above error message, because there will be two tank T1 in B2. In such case first rename the T1 tank in B1 using the **Manage Storage** form and then proceed with the movement.

```
Duplicate key violation. Record already exists in database
```

This error message is shown when you try to insert a new record which contains a unique identifier already stored in the database. For example: this can be inserting a new protocol with the same name as an existing one, or trying to insert for the second time the same animal or sample.

```
Empty samples storage identifier
 No such sample in this location
```

This error message is shown when you try to delete via the **Samples Distribution** form a record, which is already deleted. This can happen, if somebody else has erased the same record shortly before you click the **Delete** button, or if you click the **Delete** button a second time after deletion.

```
Trying to put sample twice in the same location
```

This error message is shown when you try to insert a sample via the **Sample** form, but have entered two times the same location.

```
Cannot open DS33.dat file in /tmp for writing
```

This error message is shown when you try to export data for EFABIS via the respective form, but CryoWEB cannot write the exported data to temporary file on the server. This can happen, if there is no enough space on the server, or the access permissions of the /tmp folder do not allow writing there.

```
The species of the animal and the ancestor are different
```

This error message is shown when you try to insert or update animal data via the **Animal** form, and the sire, or dam species differ from the one of the animal. The reason may be wrong sire or dam identification, wrong species data for sire, dam, or for the animal itself.

```
Do not delete the last value in the class
```

This error message is shown when you try to delete a value via the **Codes** form, but this is the last value in a class. CryoWEB prevents such deletion, as the access to the class category will be lost and the respective drop-down list broken.

```
The file is empty, does not exist, or was not uploaded
```

This error message is shown when you try to upload a file, but on the server side the file is empty. The reason may be that you are trying to upload an empty file, or there is a communication problem with the server. If the file is not empty, try to upload it again.

```
Cannot insert the protocol file in the database
```

This error message is shown when you try to upload a new protocol file via the **Protocols** form, but the software cannot store it in the database. The reason may be not enough space, or communication problem with the database engine. Try to upload the protocol file again.

```
Cannot update the protocol file in the database
```

This error message is shown when you try to update a protocol file via the **Protocols** form, but the software cannot store it in the database. The reason may be not enough space, or communication problem with the database engine. Try to upload the protocol file again. See your sysadmin about the space issue.

```
Cannot insert protocol without uploaded file
```

This error message is shown when you try to insert a new protocol record without supplying a file with the protocol data.

```
The file is not in one of the allowed image formats: JPG, PNG, GIF,
    BMP
```

This error message is shown when you try to upload animal photo via the **Animal** form, but the file is not in one of the accepted formats. CryoWEB accepts only photos in JPG, PNG, GIF or BMP format. Convert your image to one of the listed formats and upload again.

```
Cannot insert the image file in the database
```

This error message is shown when you try to upload new animal photo via the **Animal** form, but the software cannot store it in the database. The reason may be not enough space, or communication problem with the database engine. Try to upload the image again. See your sysadmin about the space issue.

```
Cannot update the image file in the database
```

This error message is shown when you try to update the animal photo via the **Animal** form, but the software cannot store it in the database. The reason may be not enough space, or communication problem with the database engine. Try to upload the image again. See your sysadmin about the space issue.

```
Cannot insert the file in the database
```

This error message is shown when you try to upload new archive for a animal via the **Animal** form, but the software cannot store it in the database. The reason may be not enough space, or communication problem with the database engine. Try to upload the archive file again. See your sysadmin about the space issue.

```
Cannot update the file in the database
```

This error message is shown when you try to update the animal archive file via the **Animal** form, but the software cannot store it in the database. The reason may be not enough space, or communication problem with the database engine. Try to upload the archive file again. See your sysadmin about the space issue.

10 Appendix

Acknowledgements

Developers

There were many people involved in the design and the implementation of the system:

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- Jutta Moosdorf
- Lina Yordanova

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List of Figures

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Index